Plasmid sequence of pNC5LSPCEAp53 (pMC30B5) for vCP2086

	1	GCCCTTT CGTCTCG CGCGTTT CGGTGAT GACGGTG AAAACCT CTGACAC ATGCAGC TCCCGGA GACGGT	С
5	_	CGGGAAA GCAGAGC GCGCAAA GCCACTA CTGCCAC TTTTGGA GACTGTG TACGTCG AGGGCCT CTGCCA	G
-	71	ACAGCTT GTCTGTA AGCGGAT GCCGGGA GCAGACA AGCCCGT CAGGGCG CGTCAGC GGGTGTT GGCGGG	T
	•	TGTCGAA CAGACAT TCGCCTA CGGCCCT CGTCTGT TCGGGCA GTCCCCC GCAGTCG CCCACAA CCGCCC	A
	141	GTCGGGG CTGGCTT AACTATG CGGCATC AGAGCAG ATTGTAC TGAGAGT GCACCAT ATGCGGT GTGAAA	T
		CAGCCCC GACCGAA TTGATAC GCCGTAG TCTCGTC TAACATG ACTCTCA CGTGGTA TACGCCA CACTTI	A
10	211	ACCECAC AGATECE TAAGGAG AAAATAC CECATCA GECECCA TTCGCCA TTCAGGC TGCGCAA CTGTTG	G
		TGGCGTG TCTACGC ATTCCTC TTTTATG GCGTAGT CCGCGGT AAGCGGT AAGTCCG ACGCGTT GACAAC	C
	281	GAAGGGC GATCGGT GCGGGCC TCTTCGC TATTACG CCAGCTG GCGAAAG GGGGATG TGCTGCA AGGCGA	T
		CITCCCG CTAGCCA CGCCCGG AGAAGCG ATAATGC GGTCGAC CGCTTTC CCCCTAC ACGACGT TCCGCT	A
	351	TAAGTTG GGTAACG CCAGGGT TITCCCA GTCACGA CGTTGTA AAACGAC GGCCAGT GCCAAGC TIGGCI	G
15		ATTCAAC CCATTGC GGTCCCA AAAGGGT CAGTGCT GCAACAT TTTGCTG CCGGTCA CGGTTCG AACCGA	C
			c
			ft Arm
	421	CAGGTAT TCTAAAC TAGGAAT AGATGAA ATTATGT GCAAAGG AGATACC TTTAGAT ATGGATC TGATTT	
20		GTCCATA AGATTIG ATCCTTA TCTACTI TAATACA CGTTTCC TCTATGG AAATCTA TACCTAG ACTAAA	.1
20	491	Left Arm TITTGGIT TITCATA ATCATAA TCTAACA ACATTIT CACTATA CTATACC TTCTIGC ACAAGIC GCCATI	מי
	431	AAACCAA AAAGTAT TAGTATT AGATTGT TGTAAAA GTGATAT GATATGG AAGAACG TGTTCAG CGGTAF	T
		Left Arm	-
	561	GTAGTAT AGACTTA TACTTTG TAACCAT AGTATAC TITAGCG CGTCATC TTCTTCA TCTAAAA CAGATT	T
25	001	CATCATA TOTGAAT ATGAAAC ATTOGTA TOATATG AAATOGO GCAGTAG AAGAAGT AGATTIT GTOTAA	
		Left Arm	
	631	ACAACAA TAATCAT CGTCGTC ATCTTCA TCTTCAT TAAAGTT TTCATAT TCAATAA CITTCIT ITCTA	A
		TGTTGTT ATTAGTA GCAGCAG TAGAAGT AGAAGTA ATTTCAA AAGTATA AGTTATT GAAAGAA AAGAT	T
		Left Arm	
30	701	ACATCAT CTGAATC AATAAAC ATAGAAC GGTATAG AGCGTTA ATCTCCA TTGTAAA ATATACT AACGCC	
		TGTAGTA GACTTAG TTATTTG TATCTTG CCATATC TCGCAAT TAGAGGT AACATTT TATATGA TTGCGC	A
		Left Arm	_
	771	TGCTCAT GATGTAC TITTTTT CATTATT TAGAAAT TATGCAT TITAGAT CTTTATA AGCGGCC GTGATT	
25		ACGASTA CTACATG AAAAAAA GTAATAA ATCTTTA ATACGTA AAATCTA GAAATAT TOGCOGG CACTAI	T
35		Toda Arm	
	841	Left Arm ACTAGTC ATAAAAA CCCGGGA TCGATTC TAGACTC GAGATAA AAACTAT ATCAGAG CAACCCC AACCAC	·C
	841	TGATCAG TATTITT GGGCCCT AGCTAAG ATCTGAG CTCTATT TITGATA TAGTCTC GTTGGGG TTGGTC	
			•
40		CEA	
40			Val·
40	911	CEA ***Ile LeuAla ValGly ValLeu ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTC	A
40	911	CEA ***Ile LeuAla ValGly ValLeu	A
	911	CEA . ***Ile LeuAla ValGly ValLeu ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTC TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA	A T
40 45		CEA ***Ile LeuAla ValGly ValLet ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTC TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metile GlyValThr AlaGly AlaSer LeuGlyPro SerThr GlySer AlaSerVal Thri	A T
	911 981	CEA ***Ile LeuAla ValGly ValLet ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTC TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metlle GlyValThr AlaGly AlaSer LeuGlyPro SerThr GlySer AlaSerVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGTTAG AGACAAA ACAGGCA TAGGTCC CGTTAN	A T le· T
		CEA ****Ile Leuala Valgly Vallet ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TCACGAG ACTGTX TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metile GlyValthr AlaGly Alaser LeuglyPro Serthr GlySer AlaserVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGTTAG ACACAAA ACAGGCA TAGGTCC CGTTAT ACGAGAA CTGATAC CTTAATA ACGCCGG TCATCGG TTCAATC TCTGTTT TGTCCGT ATCCAGG GCAATA	A T le· T
		CEA ****Ile LeuAla ValGly ValLeu ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TCAGGAG ACTGTC TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metlle GlyValThr AlaGly AlaSer LeuGlyPro SerThr GlySer AlaSerVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGGTCA ACAGGCA TAGGTCC CGTTATA ACGAGAA CTGATAC CTTAATA ACGCCGG TCATCGG TCTCATCG TCCAGG GCAATA CEA	A T le· T A
45	981	CEA ****Ile LeuAla ValGly ValLeu ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTC TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC .Glylle Metlle GlyValThr AlaGly Alaser LeuGlyPro SerThr GlySer AlaserVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGTTAG AGACAAA ACAGGCA TAGGTCC CGTTAA ACGAGAA CTGATAC CTTAATA ACGCCGG TCATCGG TTCAATC TCTGTTT TGTCCGT ATCCAGG GCAATA CEA .SerLys VallleSer AsnAsn ArgGly ThrAlaLeu AsnSer ValPhe CysAlaTyr ThrGly AsnAs	A T le· T A
		CEA ***Ile Leuala Valgly Vallet ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTY TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metile GlyValthr AlaGly Alaser LeuGlyPro Serthr Glyser AlaserVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGTTAG AGACAAA ACAGGCA TAGGTCC CGTTAT ACGAGAA CTGATAC CTTAATA ACGCCGG TCATCGG TTCAATC TCTGTTT TGTCCGT ATCCAGG GCAATT CEA .Serlys Vallleser AsnAsn ArgGly ThrAlaLeu AsnSer ValPhe CysAlaTyr ThrGly AsnAs ATTTGGC GTGATTT TGGCGAT AAAGAGA ACTTGTG TGTGTTG CTGCGGT ATCCCAT TGATACG CCAAGGATAC CCAAGGATAC CTGATAC CCAAGACAAA ACTGTGTG TGTGTTG CTGCGGT ATCCCAT TGATACG CCAAGGATACCCAAGGACAAAAAAAAAA	A T le· T A n
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45	981	CEA ***Ile Leuala Valgly Vallet ACTCCAA TCATGAT GCCGACA GTGGCCC CAGCTGA GAGACCA GGAGAAG TTCCAGA TGCAGAG ACTGTY TGAGGTT AGTACTA CGGCTGT CACCGGG GTCGACT CTCTGGT CCTCTTC AAGGTCT ACGTCTC TGACAC CEA Glylle Metile GlyValthr AlaGly Alaser LeuGlyPro Serthr GlySer AlaserVal Thri TGCTCTT GACTATG GAATTAT TGCGGCC AGTAGCC AAGTTAG AGACAAA ACAGGCA TAGGTCC CGTTAT ACGAGAA CTGATAC CTTAATA ACGCCGG TCATCGG TTCAATC TCTGTTT TGTCCGT ATCCAGG GCAATA CEA .Serlys Vallleser AsnAsn ArgGly ThrAlaLeu AsnSer ValPhe CysAlaTyr ThrGly AsnAs ATTTGGC GTGATTT TGGCGAT AAAGAGA ACTTGTG TGTGTTG CTGCGGT ATCCCAT TGATACG CCAAGA TAAACCG CACTAAA ACCGCTA TTTCTCT TGAACAC ACACAAC GACGCCA TAGGGTA ACTATGC GGTTCT CEA AsnProthr Ilelys Alaile Pheleuval Ginthr HisGin GinProile GlyAsn IleArg TrySer TACTGCG GGGATGG GTTAGAG GCCGAGT GGCAGGA GAGGTTG AGGTCCG CTCCCGA AAGGTAA GACGAC	A T T T A II T Tyr
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ASSESTED ILESET PROLYS PROLEUGIU Alaser ValThr IleThrLys ValThr ThrArg Seri CCACTGG CTGGATT ATTGGCC TAGCAGA TATAGGG TCCGCTG TTCTTCT CAGTTAT GTTGCTT ATAGGT GTGCTA TATAGGG TCGACT ATACCGG ACCGTG TTCTTCT CAGTTAT GTTGCTT ATAGGT ATACCAGA TATACCGG ACCGTG ATACCAGAGA TATCCAGAGAGA TATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	TAT TAT TELEU TIGC TAGA TAGA TAGA TAGA TAGA TAGA TAGA TA
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Hiscysser Leuser Leusen Valglypro Argyyr TyrThr TyrSerPro Serile ThrPro Asple GGGCCAT ACAAAAC ATTAAGG ATAACAG GGTCGGA GTGATCA ACGGATA ATTCATT CTGAARG CACCGGTA TGTTTTG TAATTCC TATTGTC CCAGCCT CACTAGT TACGTAA ATTCATC CCAGCGT CACTAGT TACGTAA GACTTAC GGT CATAGGT TAGTTAC GATAGGTAA TCATAGG TCCTACA TCATTGC GAGTAAC GGACAGG AGTGTCA ATGTGCG GTTATCA TTAGACA ACT GTATTCC AGGATGT AGTACG GAGTAAC GGACAGG AGTGTCA ATGTGCG GTTATCA TTAGACA ACT GTATTCC AGGATGT AGTACG GAGTAAC GGACAGG AGTGTCA ATGTGCG GTTATCA TTAGACA ACT CAA ACT CACAGT TACACGC CAATAGT AATCTGT TGAACCT TCACAGT TACACGC CAATAGT AATCTGT TGAACCT TCACAGT TACACGC CAATAGT AATCTGT TGAACCT TCACAGT TACACGC CAATAGT AATCTGT TGAACCT TAGACCA ACACGAAC AATCAGG TGGATAT TATCAC CATAAAA CTTAGAAC ACCGAAC AACACGAAC AACACGA AACACGA TACACGG TGGATAT TATCAC CATAAAA CTTAGAAC ACCGAAC AACACGAA AACTGGG TGGATAT TATCAC CATAAAA CTTAGAAC ACCGAAC AACACGAA AACTGGG TGGAACT TATCAC CATAAAA CTTAGAAC ACCGAAC AACACGAA AACTGGA GTTAGAA TGCAACA TACACAC TCACCTA AACACGA TACACAG GTTAGAA TGCAACA TACACACA TACACTG GTTAGAA TGCAACA TACACACA TACACTG GTTAGAA TACAATA ACCAATA ACCACATA AACACGA AACACGA AACACGA CAACACAC CAACACAC AACACGA AACACAC CAACACAC CAACACAC CAACACAC CAACACAC CAACACAC CAACACAC CACACAC CAACACAC CACACAC CAACACAC CACACAC CA	ACT FTGA ysGlu· SCAA CGTT ALeu CTCA GAGT GAGT GluCys·
CATARGE TCCTACA TCATTGC GAGTRAC GEACAGG AGTGTCA ATGTGGG GTTATCA TTAGACA ACT GTATTCC AGGATGT AGTARCG CTCATTG CCTGTCC TCACAGT TACACGC CAATAGT AATCTGT TCA CEA .TyrPro GlyValasp Asnarg ThrVal SerLeuLeu ThrLeu ThrArg Asnaspasn SerLeu Gl GCGTGGG CTAACCG GCAAACT TTGGTTA TTGACCC ACCATAA ATAAGTG GTATTT GAATCTC TGC CCCACCC GATTGGC CGTTTGA AACCAAT AACTGGG TGGTATT TATTCAC CATAAAA CTTAGAG ACC CEA ArgProSer ValPro LeuSer GlnAsnasn ValTrp TrpLeu TyrThrThr AsnGln IleGlu Pro CEA ArgProSer ValPro LeuSer GlnAsnasn ValTrp TrpLeu TyrThrThr AsnGln IleGlu Pro CEA ArgProSer ValPro LeuSer GlnAsnasn ValTrp TrpLeu TyrThrThr AsnGln IleGlu Pro CEA ArgProSer ValPro LeuSer GlnAsnasn ValTrp TrpLeu TyrThrThr AsnGln IleGlu Pro CEA ThrLeu AlaVal AlaAspGlu AspGlu ValPro AsnSerAsn AsnSer ThrIle PheProLys I CEA ThrLeu AlaVal AlaAspGlu AspGlu ValPro AsnSerAsn AsnSer ThrIle PheProLys I CEA GluTyr ValThrIle ThrThr ValThr ThrArgAsn LeuGly ThrAsp SerAsnAs Actogat CCC CEA GluTyr ValThrIle ThrThr ValThr ThrArgAsn LeuGly ThrAsp SerAsnAs Actogat CATCCTA GGTGATA ACCATCT ACTTGT AACCAT TACTCGG GTGGAC GTGGAC GTGGAC CATCCTA GGTGATA ACCATCT ACTTGT AACCAT ACCATCA CACCTT TO CEA 100 101 102 103 103 104 105 105 106 107 107 107 107 107 107 107	CCAA CGTT DLeu CTCA GAGT GluCys - GGTG
25 1691 GCGTGGG CTAACCG GCAAACT TTGGTTA TTGACCC ACCATAA ATAAGTG GTATTTT GAATCTC TGCGCACCC GATTGGC CGTTTGA AACCAAT AACTGGG TGGTATT TATTCAC CATAAAA CTTAGAG ACCCCCCCCCC	GAGT GluCys - CGTG
1961 CAAGTTA ATGCAAC TGCGTCC TCATCCT CAACTGG GTTAGAA TTGTTAC TAGTTAT GAATGGT TTT 30 GTTCAAT TACGTTG ACGCAGG AGTAGGA GTTGACC CAATCTT AACAATG ATCAATA CTTACCA AAA ThrLeu AlaVal AlaAspGlu AspGlu ValPro AsnSerAsn AsnSer ThrIle PheProLys I CEA 2031 GCTCATA CACGGTA ATCGTCG TCACGGT TGTGCGG TTGAGTC CGGTGTC GCTATTG TGAGCTT GGG CGAGTAT GTGCCAT TAGCAGC AGTGCCA ACTCAG GCCACAG CGATAAC ACTCGAA CCC 2101 GTAGGAT CCACTAT TGTTCAC GGTAATA TTGGGAA TGAACAG TTCCTGG GTGGACT GTTGGAA AGT CATCCTA GGTGATA ACAAGTG CCATTAT AACCCTT ACTTGTC AAGGACC CACCTGA CAACCTT TCA 2101 TYPSERGLY SERASN ASNVAL THRILEASN PROILE PHELEU GLUGINTHY SERGIN GINPHE THR 2171 TTGACAA ACCAGCT GTATTGG GCGGGAG GATTGCT AGCGGCA TGACAGC TCAGATT CAGATTT TCAACGA TCGCCGT ACTGTCG AGTCTAA AGCACG 2241 ACCTATA GCTTGTG TTTAGAG GGCTGAT TGTAGGA GCATCGG GTCCGTA AAGCACG TTGAGAA TCGCAGAT TCGAGATT CGAACAC AAATCTC CCGACTA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGCACAC TCGAGAT TCGAGAA TCGCCGG GTCCGTA AAGCACG TTGAGAA TCGCAGAA TCGCCGG GTCCGTA AAGCACG TTGAGAA TCGCAGAT TCGAGAAT TCGAGAAT TCGAGAAT TCGAGAAT TCGAGAAT TCGAGAAT TCGAGAAT TCGAGAAT AAGCACG TTGAGAA TCGCAGAT TTGAGAA TCGCCGAATAA AGCACG TTGAGAA TCGCAGAT TCGAGAAT T	GGIG
2031 GCTCATA CACGGTA ATCGTCG TCACGGT TGTGCGG TTGAGTC CGTGTCT GCTATTG TGAGCTT GGG CGAGTAT GTGCCAT TAGCAGC AGTGCCA ACACGCC AACTCAG GCCACAG CGATAAC ACTCGAA CCC 2101 GTAGGAT CCACTAT TGTTCAC GGTAATA TTGGGAA TGAACAG TTCCTGG GTGGACT GTTGGAA AGT CATCCTA GGTGATA ACAGGTG CCATTAT AACCCTT ACTTGTC AAGGACC CACCTGA CAACCTT TCACACACAT TGTGCAA ACAGGTG CATCAGA ACAGGTG CACCTGA CAACCTT TCACACAA ACCAGCT GTATTGG GCGGAG GATTGCT AGCGGCA TGACAGC TCAGATT CAGATTT TCACACAA ACCAGCT GTATTGG GCGGAG GATTGCT AGCGGCA TGACAGC TCAGATT CAGATTT TCACACAA ACCAGCT TGGTCGA CATCACAA TCGCCGT ACTGTCG AGTCTAA AGCACG TCAACAA ACCAGCT TGAGAA TCGCCGA TACACGA TCGCCGA ACCTCTAA AGCACG TCAGATT CAGATTT TCGACAA ACCAGCT TGAGGAA TCGCCGA ACTGTCG GTCCGTA AAGCACG TTGAGAA TCGCCGAT AAGCACG TTGAGAA TCGCCGATAA AGCACG TTGAGAA TCGCCGATAA ACATCCT CGTAGCA CAACCCT TCGTGC AACTCTT AGCACCA TTGAGAA TCGCCGATAA AAGCACG TTGAGAA TCGCCGATAA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGCACCACACACACACACACAAAACCC CCGACTA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGCACCACACACACACACACACACACACAAAACCC CCGACTAA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGCACACACACACACACACACACACACACACACACACAC	
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2171 TTGACAA ACCAGCT GTATTGG GCGGGAG GATTGCT AGCAGC TCAGATT CAGATT TCCAGATT TGGTCGA CATAACC CGCCCTC CTAGACGA TCGCCGT ACTGTCG AGTCTAA AGCACC CEA Valphe Trpser Tyrglnala Propro Asnser Alaalahis Cysser Leuasn Leuasnglu (ATCTATA GCTTGTG TTTAGAG GGCTGAT TGTAGGA GCATCGG GTCCGTA AAGCACG TTGAGAA TCC TAGATAT CGAACAC AAATCTC CCGACTA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGCACCC CEACCCCCCCCCCCCCCCCCCCCCCCCCCCC	GCCA CGGT
45 2241 ATCTATA GCTTGTG TTTAGAG GGCTGAT TGTAGGA GCATCGG GTCCGTA AAGCACG TTGAGAA TCC TAGATAT CGAACAC AAATCTC CCGACTA ACATCCT CGTAGCC CAGGCAT TTCGTGC AACTCTT AGC CEA	GGAC
	CIGA GACT
Argtyr Serthrasn Leupro Serile Thrproala Asppro GlyTyr Leuvalasn Leuile Volume 1	CACG GTGC
AspSerArg ArgAla SerVal ProAsnGln ThrGlu CysLys TyrSerAla ThrAsp AsnArg Thr 2381 TTAAACA GGGTCAG AGTTCTA TTTCCGT TGCTGAG TTGGAGT CTAGGGG ACACAGG CAGGGAC TGC AATTTGT CCCAGTC TCAAGAT AAAGGCA ACGACTC AACCTCA GATCCCC TGTGTCC GTCCCTG ACC 55	AACA
PheLeu ThrLeu Thrargasn GlyAsn SerLeu GlnLeuArg ProSer ValPro LeuSerGln 2 TCACCCA CCAGAGA TATGTTG CGTCTTG AGTTTCG GGCTCGC ATGTAAA AGCGACG GCATCTT TG AGTGGGT GGTCTCT ATACAAC GCAGAAC CCAGAGC GTACATTT TCGCTGC CGTAGAA ACC	GAAG
O .Valtrp Trpleutyr Thrala AspGln ThrGluPro GluCys ThrPhe AlaValala AspLys A. GACAGGC TTACTAT TATTGGA GCTAATA GAAGGCT TAGGGAG TTCCGGG TATACCC GGAACTG GCC CTGTCCG AATGATA ATAACCT CGATTAT CTTCCGA ATCCTC AAGGCCC ATATGGG CCTTGAC CGCA CEA	AGTT
Valprolys Serasm Asmser SerileSer Frolys ProLeu GluproTyr Valarg PheGlm Gl: 65 2591 GCTTCTT CATTCAC AAGATCT GACTTTA TGACGTG TAGGGTG TAGAATC CTGTGTC ATTCTGG ATC CGAAGAA GTAAGTG TTCTAGA CTGAAAT ACTGCAC ATCCCAC ATCTTAG GACACAG TAAGACC TAGACC CEA	
GluGlu AsnVal LeuAspSer LysIle ValHis LeuThrTyr PheGly ThrAsp AsnGlnIle : 2661 TCTGGAT CAGCAGG GATGCAT TGGGGTA TATTATC TCTCGAC CACTGTA TGCGGGC CCTGGGG TAGAGACTA GTCGTCC CTACGTA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG GGACCCC ATGCAGA ACCCCAT CTACGTA ACCCCCAT CTACGTA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG GGACCCC ATGCAGA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG GGACCCC ATGCAGA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG GGACCCC ATGCAGA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG ATGCAGA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG ATGCAGA ACCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG ATGCAGA ACCCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCG ATGCAGA ACCCCCAT ATAATAG AGAGCTG GTGACAT ACGCCCC ATGCAGA ACCCCCAT ATAATAG AGAGCTG ATGCAGA ACGCCCC ATGCAGA ACCCCCAT ATAATAG AGAGCTG ATGCAGA ACGCCCC ATGCAGA ACCCCCAT ATAATAG AGAGCTG ATGCAGA ACGCCCC ATGCAGA ACCCCAT ATAATAG AGAGCTG ATGCAGA ACGCCCC ATGCAGA ACGCCCC ATGCAGA ACCCCAT ATGCAGA ACGCCCC ATGCAGA ACCCCCAT ATGCAGA ACCCCCAT ATGCAGA ACGCCCC ATGCAGA ACCCCCAT ATGCAGA ACCCCAT ATGCAGA ATGCAGA ATGCAGA ATGCAGA ATGCAGA ATGCAGA ATGCAGA ATGCAGA ATG	ThrAla· ATGT TACA
Glnile Leuleuser Alaasn Protyr Ileileglu Arggly Sertyr Alaprogly Prothr Alaprogly Communication of the Alaprogram of the	ThrAla. HATGT TACA LeAsn. CTTG GAAC

		CEA
5	2801	GINTHYGLY ILEVAL TYYGLY ILELLEGIN AYGASH GLYASP VALAYGGLU GLYLYS TYYTYP SETTYYGLY. CCARARA GATGCTG GGCCACA TTGTGGA CAAGTAG AAGCACC TCCTTCC CCTCTGC GACATTG AACGGCG GGTTTTT CTACGAC CCCGTCT AACACCT GTTCATC TTCGTGG AGGAAGG GGAGACG CTGTAAC TTGCCGC CEA
J	2871	PheLeu HisGln ProLeuasn HisVal LeuLeu LeuValGlu LysGly Gluala ValasnPhe ProThr. TGGATTC AATAGTG AGCTTGG CAGTGGT GGGCGGG TTCCAGA AGGTTAG AAGTGAG GCTGTGA GCAGGAG ACCTAAG TTATCAC TCGAACC GTCACCA CCCGCCC AAGGTCT TCCAATC TTCACTC CGACACT CGTCCTC CEA
10	2941	Serglu IleThrleu Lysala ThrThr Proproasn TrpPhe Thrleu LeuSerala Thrleu LeuLeu CCTCTGC CAGGGGA TGCACCA TCTGTGG GGAGGGG CCGAGGG AGACTCC ATTATTT ATATTCC AAAAAAA GGAGACG GTCCCCT ACGTGGT AGACACC CCTCCCC GGCTCCC TCTGAGG TAATAAA TATAAGG TTTTTTT
15		R/L Promoter
13		CEA
		ArgGlnTrp ProIle CysTrp ArgHisPro ProAla SerPro SerGluMet H6 promoter
20	3011	AAAAATA AAATTTC AATTTTT GTCGACC TGCAGCT CGACGGA TCCCCCC GGGTTCT TTATTCT ATACTTA TTTTTAT TTTAAAG TTAAAAA CAGCTGG ACGTCGA GCTGCCT AGGGGGG CCCAAGA AATAAGA TATGAAT
		E/L Promoter H6 promoter
25		
	3081	AAAAGTG AAAATAA ATACAAA GGTTCTT GAGGGTT GTGTTAA ATTGAAA GGGAGAA ATAATCA TAAATTA TTTTCAC TTTTATT TATGTTT CCAAGAA CTCCCAA CACAATT TAACTTT CGCTCTT TATTAGT ATTTAAT p53
30		H6 promoter
		MetGlu GluProGln SerAsp ProSer ValGluPro
25	3151	TTTCATT ATCGCGA TATCCGT TAAGTTT GTATCGT AATGGAG GAGCCGC AGTCAGA TCCTAGC GTCGAGC AAAGTAA TAGCGCT ATAGGCA ATTCAAA CATAGCA TTACCTC CTCGGCG TCAGTCT AGGATCG CAGCTCG
35		p53
40	3221	ProLeu SerGln GluthrPhe SerAsp Leutrp LysLeuLeu ProGlu AsnAsn ValleuSer ProLeu CCCCTCT GAGTCAG GAAACAT TITCAGA CCTATGG AAACTAC TITCCTGA AAACAAC GTTCTGT CCCCCTT GGGGAGA CTCAGTC CTTTGTA AAAGTCT GGATACC TITGATG AAGGACT TITGTTG CAAGACA GGGGGAA p53
45	3291	Proser Ginalamet Aspasp Leumet Leuserfro Aspasp Ilegiu Gintyphe Thrgiu Aspfro GCCGTCC CAAGCAA TGGATGA TTTGATG CTGTCCC CGGACGA TATTGAA CAATGGT TCACTGA AGACCCA CGGCAGG GTTCGTT ACCTACT AAACTAC GACAGGG GCCTGCT ATAACTT GTTACCA AGTGACT TCTGGGT p53
73		
50	3361	GlyProAsp Gluala ProArg MetProGlu AlaAla ProPro ValalaPro AlaPro AlaAla ProThrPro- GGTCCAG ATGAAGC TCCCAGA ATGCCAG AGGCTGC TCCCCCC GTGGCCC CTGCACC AGCAGCT CCTACAC CCAGGTC TACTTCG AGGGTCT TACGGTC TCCGACG AGGGGGG CACCGGG GACGTGG TCGTCGA GGATGTG p53
55	3431	AlaAla ProAla ProAlaPro SerTrp ProLeu SerSerSer ValPro SerGln LysThrTyr GlnGly- CGGCGGC CCCTGCA CCAGCCC CCTCCTG GCCCCTG TCATCTT CTGTCCC TTCCCAG AAAACCT ACCAGGG GCCGCCG GGGACGT GGTCGGG GGAGGAC CGGGGAC AGTAGAA GACAGGG AAG
55		
60	3501	SerTyr GlyPheArg LeuGly PheLeu HisSerGly ThrAla LysSer ValThrCys ThrTyr SerPro CAGCTAC GGTTTCC GTCTGGG CTTCTTG CATTCTG GGACAGC CAAGTCT GTGACTT GCACGTA CTCCCCT GTCGATG CCAAAGG CAGACCC GAAGAAC GTAAGAC CCTGTCG GTTCAGA CACTGAA CGTGCAT GAGGGGA p53
65	3571	AlaLeuAsn LysMet PheCys GlnLeuAla LysThr CysPro ValGlnLeu TrpVal AspSer ThrProPro- GCCCTCA ACAAGAT GTTTTGC CAACTGG CCAAGAC CTGCCCT GTGCAGC TGTGGGT TGATTCC ACACCCC CGGGAGT TGTTCTA CAAAACG GTTGACC GGTTCTG GACGGGA CACGTCG ACACCCA ACTAAGG TGTGGGG p53
70	3641	ProGly ThrArg ValArgAla MetAla IleTyr LysGlnSer GlnHis MetThr GluValVal ArgArg. CGCCCGG CACCGC GCCCGC CCATGGC CATCTAC AAGCAGT CACAGCA CATGACG GAGGTTG TGAGGCG GCGGGCC GTGGGCG CATGCCG GTAGATG TTCGTCA GTGTCGT GTACTGC CTCCAAC ACTCCGC p53
	3711	.CysPro HisHisGlu ArgCys SerAsp SerAspGly LeuAla ProPro GlnHisLeu IleArg ValGlu CTGCCCC CACCATG AGCGCTG CTCAGAT AGCGATG GTCTGGC CCCTCCT CAGCATC TTATCCG AGTGGAA GACGGGG GTGGTAC TCGCGAC GAGTCTA TCGCTAC CAGACCG GGGAGGA GTCGTAG AATAGGC TCACCTT

p53

5	3781	GlyAsnLeu ArgVal GluTyr LeuAspAsp ArgAsn ThrPhe ArgHisSer ValVal ValPro TyrGluPro- GGAAATT TGCGTGT GGAGTAT TTGGATG ACAGAAA CACTTTT CGACATA GTGTGGT GGTGCCC TATGAGC CCTTTAA ACGCACA CCTCATA AACCTAC TGTCTTT GTGAAAA GCTGTAT CACACCA CCACGGG ATACTCG p53
10	3851	ProGlu Valgly Seraspcys ThrThr IleHis TyrasnTyr Metcys AsnSer SerCysMet GlyGly. CGCCTGA GGTTGGC TCTGACT GTACCAC CATCCAC TACAACT ACATGTG TAACAGT TCCTGCA TGGGCGG GCGGACT CCAACCG AGACTGA CATGGTG GTAGGTG ATGTTGA TGTACAC ATTGTCA AGGACGT ACCCGCC p53
15	3921	Metasn Argargpro Ileleu Thrile IleThrleu Gluasp SerSer Glyasnleu Leugly Argasn Catgaac CGGAGGC CCATCCT CACCATC ATCACAC TGGAAGA CTCCAGT GGTAATC TACTGGG ACGGAAC GTACTTG GCCTCCG GGTAGGA GTGGTAG TAGTGTG ACCTTCT GAGGTCA CCATTAG ATGACCC TGCCTTG p53
20	3991	SerPheGlu ValArg ValCys AlaCysPro GlyArg AspArg ArgThrGlu GluGlu AsnLeu ArgLysLys. AGCTTTG AGGTGCG TGTTTGT GCCTGTC CTGGGAG AGACCGG CGCACAG AGGAAGA GAATCTC CGCAAGA TCGAAAC TCCACGC ACAAACA CGGACAG GACCCTC TCTGGCC GCGTGTC TCCTTCT CTTAGAG GCGTTCT p53
25	4061	GlyGlu ProHis HisGluLeu ProPro GlySer ThrLysArg AlaLeu ProAsn AsnThrSer SerSer- AAGGGGA GCCTCAC CACGAGC TGCCCCC AGGAGC ACTAAGC GAGCACT GCCCAAC AACACCA GCTCCTC TTCCCCT CGGAGTG GTGCTCG ACGGGGG TCCCTCG TGATTCG CTCGTGA CGGGTTG TTGTGGT CGAGGAG p53
30	4131	ProGln ProLysLys LysPro LeuAsp GlyGluTyr PheThr LeuGln IleArgGly ArgGlu ArgPhe TCCCCAG CCAAAGA AGAAACC ACTGGAT GGAGAAT ATTTCAC CCTTCAG ATCCGTG GGCGTGA GCGCTTC AGGGGTC GGTTTCT TCTTTGG TGACCTA CCTCTTA TAAAGTG GGAAGTC TAGGCAC CCGCACT CGCGAAG p53
35	4201	GluMetPhe ArgGlu LeuAsn GluAlaLeu GluLeu LysAsp AlaGlnAla GlyAys GluPro GlyGlySer- GAGATGT TCCGAGA GCTGAAT GAGGCCT TGGAACT CAAGGAT GCCCAGG CTGGGAA GGAGCCA GGGGGGA CTCTACA AGGCTCT CGACTTA CTCCGGA ACCTTGA GTTCCTA CGGGTCC GACCCTT CCTCGGT CCCCCCT p53
40	4271	Argala Hisser SerHisleu Lysser Lyslys GlyGlnSer ThrSer ArgHis LysLysLeu MetPhe- GCAGGGC TCACTCC AGCCACC TGAAGTC CAAAAAG GGTCAGT CTACCTC CCGCCAT AAAAAAC TCATGTT CGTCCCG AGTGAGG TCGGTGG ACTTCAG GTTTTTC CCAGTCA GATGGAG GGCGGTA TTTTTTG AGTACAA p53
45	4341 4411	LIYSTHY GLUGLYPYO ASPSEY ASP*** CAAGACA GAAGGGC CTGACTC AGACTGA ACGCGTT TTTTATC CCGGGCT CGAGGGT ACCGGAT CCTTTTT GTTCTGT CTTCCCG GACTGAG TCTGACT TGCGCAA AAAATAG GGCCCGA GCTCCCA TGGCCTA GGAAAAA ATAGCTA ATTAGTC ACGTACC TTTGAGG GTACCAC TTCAGCT ACCTCTT TTGTGTC TCAGAGT AACTTTC TATCGAT TAATCAG TGCATGG AAACTCT CATGGTG AAGTCGA TGGACAA AACACAG AGTCTCA TTGAAAG
50	4481	Right Arm TTTAATC AATTCCA AAACAGT ATATGAT TTTCCAT TTCTTTC AAAGATG TAGTTTA CATCTGC TCCTTTG AAATTAG TTAAGGT TTTGTCA TATACTA AAAGGTA AAGAAAG TTTCTAC ATCAAAT GTAGACG AGGAAAC Right Arm
55	4551	TTGAAAA GTAGCCT GAGCACT TCTTTTC TACCATG AATTACA GCTGGCA AGATCAA TTTTTCC CAGTTCT AACTTTT CATCGGA CTCGTGA AGAAAAG ATGGTAC TTAATGT CGACCGT TCTAGTT AAAAAAGG GTCAAGA Right Arm GGACATT TTATTTT TTTTAAG TAGTGTG CTACATA TTTCAAT ATTTCCA GATTGTA CAGCGAT CATTAAA
	4621 4691	CCTGTAA AATAAAA AAAATTC ATCACAC GATGTAT AAAGGTA TAAAGGT CTAACAT GTCGCTA GTAATTT Right Arm CCACTAG CTCCCAT GTTATCC AGCAGGT CAGTGTATC AGCACCT TTGTTCA ATAGAAG TTTAACC ATTGTTA
60	4761	CCTCATG CAGGGTA CAATAGG TCGTTCA GTCATAG TCGTGGA AACAAGT TATCTTC AAATTGG TAACAAT Right Axm AAGTGTT AGGGCTA TATGTAG AGGAGTT AACCGAT CAGAATA TCTACAT CCGCCGA
65	4831	TTAAAAA TAAACTA TGCCGAT ATACATC TCCTCAA TTGGCTA GGCACAA ACTTTAT AGATGTA GGCGGCT Right Arm ATGAGCC AATAGAA GTTTAAC CAAATTA ACTTTGT TAAGGTA AGCTGCC AAACACA AAGGAGT AAAGCCT TACTCGG TTATCTT CAAATTG GTTTAAT TGAAACA ATTCCAT TCGACGG TTTGTGT TTCCTCA TTTCGGA
	4901	Right Arm CCGCTGT AAAGAAC ATTGTTT ACATAGT TATTCTT CAACAGA TCTTTCA CTATTTT GTAGTCG TCTCTCA GGCGACA TTTCTTG TAACAAA TGTATCA ATAAGAA GTTGTCT AGAAAGT GATAAAA CATCAGC AGAGAGT
70	4971	Right Arm ACACCGC ATCATGC AGACAAG AAGTTGT GCATTCA GTAACTA CAGGTTT AGCTCCA TACCTCA TCAAGAT TGTGGCG TAGTACG TCTGTTC TTCAACA CGTAAGT CATTGAT GTCCAAA TCGAGGT ATGGAGT AGTTCTA Right Arm
	5041	TTTTATA GCCTCGG TATTCTT GAACATT ACAGCCA TTTCAAG AGGAGAT TGTAGAG TACCATA TTCCGTG

		AAAATAT	CGGAGCC	ATAAGAA	CTTGTAA TG	roggt aaagtto	TCCTCTA	ACATCTC	ATGGTAT	AAGGCAC
				***********	Right	t Axm TTTAG AGATGCA	ማምርምር አ ጥ	ጥልጥረሃግልጥ	GATAGCC	TCACAGA
	5111	TTAGGGT	CGAATCC	ATTGTCC	AAAAACC TAT	ritag agaigce Aaatc tctacgi	DACAGTA	ATAGGTA	CTATCGG	AGTGTCT
•		AATCCCA	GCTTAGG	IAACAGG		t Arm	monoth	111100111		
5	5181	COTATAT	CTARGCC	ATCTTGA	ATGTATA ATT	TTTGT TGTTTTC	AACAACC	GCTCGTG	AACAGCT	TCTATAC
	3101	GCATATA	CATTCGG	TAGAACT	TACATAT TA	AAACA ACAAAA	TTGTTGG	CGAGCAC	TTGTCGA	AGATATG
					Richt	t Arm				
	5251	TTTTTCA	TTTTCTT	CATGATT	AATATAG TT	TACGG AATATA	GTATACA	AAAAGTT	TATAGTA	ATCTCAT
10		AAAAAGT	AAAAGAA	GTACTAA	TTATATC AA	ATGCC TTATAT	CATATGT	TTTTCAA	ATATCAT	TAGAGTA
					Right	t Arm			> maaaamm	mmma mma
	5321	AATATCT	GAAACAC	ATACATA	AAACATG GA	AGAAT TACACG	TGTCGTT	GAGATAA	MACCOAN	ANATANC
		TTATAGA	CTTTGTG	TATGTAT		TCTTA ATGTGC	ACAGCAA	CICIALI	INCCOM	NATING
15	5201	max mx am	MAIN (17.7.7.7	TTTCCCAC	אזקתי האסייה מייי	t Arm TCTTT TACGAA	ATTGCAG	AATCTGT	TTTATCC	AACCAGT
15	5391	TCATAGI	TIMCAMA	ANGOGTO	ATTAGAA GT	AGAAA ATGCTT	TAACGTC	TTAGACA	AAATAGG	TTGGTCA
					Righ	t. Arm				
	5461	GATTTTT	GTATAAT	ATAACTG	GTATCCT AT	CTTCC GATAGAZ	TGCTGTT	ATTTAAC	ATTTTTG	CACCTAT
		CTAAAAA	CATATTA	TATTGAC	CATAGGA TA	GAAGG CTATCT	ACGACAA	TAAATTG	TAAAAAC	GTGGATA
20					Righ	t. Arm				
	5531	TAAGTTA	CATCTGT	CAAATCC	ATCTTTC CA	ACTGA CTTTATO	TAACGAT	GCGAAAT	AGCATTT	ATCACTA
		ATTCAAT	GTAGACA	GTTTAGG	TAGAAAG GT	TGACT GAAATA	: ATTGCTA	CGCTTTA	TCGTAAA	TAGTGAT
					Righ	t Arm	a monwey a	mamonom	ባሃርር አጥአጥ	ጥር የርምኮ አጥ
05	5601	TGTCGTA	CCCAATT	ATCATGA	CAAGATT CT	CTTAA ATACGT GAATT TATGCA	ALCIINI	ATACACA	ACCTATA	ACCATTA
25		ACAGCAT	GGGTTAA	TAGTACT		GAATT TAIGCA LL Arm	IAGAAIA	HIMOMON	MCGININ	MCMIA
	5.623	NOWN NOWN	CTABACA	ביי איי איי א	ATANCAG TA	TAGAT ATACAC	ATATATA	AATATTT	AACCCCA	TTCCTGA
	5671	WG1WH11	GIAMAGA	CATATCC	TATTATATA	ATCTA TATGTG	ACTATAT	TTATAAA	TTGGGGT	AAGGACT
					Righ	t Arm				
30	5741	GTAAAAT	AATTACG	ATATTAC	ATTTCCT TT	TATTA TTTTTA	CTTTTAG	TTATTTG	TTAGGTT	ATACAAA
50		CATTTTA	TTAATGC	TATAATG	TAAAGGA AA	TAAAA TAATA	A CAAAATC	AATAAAC	AATCCAA	TATGTTT
					Righ	t Arm				
•	5811	AATTATG	TTTATTT	GTGTATA	TTTAAAG CG	TOGTT AAGAAT	A AGCTTAG	TTAACAT	ATTATCG	CTTAGGT
		TTAATAC	AAATAAA	CACATAT		AGCAA TTCTTA	TCGAATC	AATTGTA	TAATAGC	GAATCCA
35					Righ	t Arm		*******	COMPOND	CCAAACT
	5881	TTTGTAG	TATTTGA	ATCCTTT	CTTTAAA TG	GATTA TTTTTC	2 AAIGCAI	WILITAL	CCITCAL	CCARAGI
		AAACATC	ATAAACT	TAGGAAA		it Arm	3 IIACGIA	IMMINI	CGILIGIA	001114
	5951	ስምአስ ር ስም	יי מיי ממייי	тсасаат	TECECC CC	AATTC AATTCG	T AATCATG	GTCATAG	CTGTTTC	CTGTGTG
40	3331	TATTCTA	ATTGTA	AGTCTTA	ACGCCGG CG	TTAAG TTAAGC	A TTAGTAC	CAGTATC	GACAAAG	GACACAC
-10										
			Right	Arm						
	6021					CATAC GAGCCG	3 AAGCATA	AAGTGTA		GGGTGCC
		AAATTGT	TATCCGC	TCACAAT	TCCACAC AA				AAGCCIG	GGG3 GGG
		ጥጥጥአልሮል	ስጥስ <i>ር</i> ርርር	ልርተየርተምል ል	AGGTGTG TT	GTATG CTCGGC	TTOGTAI	TTCACAT	TTCGGAC	CCCACGG
45	6091	TTTAACA	ATAGGCG	AGTGTTA	AGGTGTG TT	GTATG CTCGGC	TTOGTAT	TTCACAT TCCAGTC	TTCGGAC	CCCACGG
45		TTTAACA TAATGAG	ATAGGCG TGAGCTA	AGTGTTA ACTCACA TGAGTGT	AGGTGTG TT TTAATTG CG	GTATG CTCGGC TTGCG CTCACT AACGC GAGTGA	C TTOGTAT C CCCCCTT C GGGCGAA	TTCACAT TCCAGTC AGGTCAG	TTCGGAC GGGAAAC CCCTTTG	CCCACGG CTGTCGT GACAGCA
45	6091 6161	TTTAACA TAATGAG ATTACTO	ATAGGCG TGAGCTA ACTCGAT	AGTGTTA ACTCACA TGAGTGT	AGGTGTG TT TTAATTG CG AATTAAC GC	GTATG CTCGGC STTGCG CTCACT ZAACGC GAGTGA SCGCGG AGAGGC	TTOGTAT CCCGCTT GGGCGAA GGTTTGCG	TTCACAT TCCAGTC AGGTCAG TATTGGG	TTCGGAC GGGAAAC CCCTTTG CGCTCTT	CCCACGG CTGTCGT GACAGCA CCGCTTC
45	6161	TTTAACA TAATGAG ATTACTC GCCAGCT CGGTCGA	ATAGGCG TGAGCTA ACTCGAT GCATTAA CGTAATT	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGGTTGC GC	TETATG CTCGGC TTGCG CTCACT TACGC GAGTGA CGGGG AGAGGC TCCCC TCTCCG TTCGGC TGCGGG	TTOGTAT CCCGCTT CCGGCGAA CGCGCAA CCCCCAAACGC CCAAACGC CAACGCCAACGCCAACGCCAACGCCAAACACAACA	TTCACAT TCCAGTC AGGTCAG TATTGGG ATAACCC TCAGCTC	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA
		TTTAACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTC	ATAGGCG TGAGCTA ACTCGAT GCATTAA CGTAATT ACTGACT	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA	AGTATG CTCGGC FITGCS CTCACT PAACGC GAGTGA ACGCGG AGAGGC TCTCGG TTCGGC TGCGGC ACGCCT ACGCGGC	C TTOGTAT C CCCGCTA C GGGCGAA G GTTTGCG C CAAACGC AGCGGTA C TCGCCAT	TTCACAT TCCAGTC AGGTCAG TATTGGG ATAACCC TCAGCTC AGTCGAG	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT
50	6161	TTTAACA TAATGAG ATTACTO GCCAGCT CGGTCGA CTCGCTC GAGCGAG	ATAGGCG TGAGCTA ACTCGAT GCATTAA CGTAATT ACTGACT TGACTGA	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG GCGACGC	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GCGGATA AC	TATATO CTCGGC STTGCS CTCACT PAACGC GAGTGA ACGCGG AGAGGC TCTCGG TCGGGC TCTCGG TCGGGC ACGCGGC ACGCGGC ACGCGGC	TTOGTAT COCCTT GGGCGAA GGTTTGCG CAAACGC AGCGGTA CTCGCCAT	TTCACAT TCCAGTC AGGTCAG TATTGGG ATAACCC TCAGCTC AGTCGAG CAAAAGG	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT AAGGCCA
	6161 6231	TTTAACA TAATGAG ATTACTO GCCAGCT CGGTCGA CTCGCTC GAGCGAG ATACGGT	ATAGGCG TGAGCTA ACTCGAT GCATTAA CGTAATT ACTGACT TGACTGA TTATCCAC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG GCGACGC AGAATCA	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GGGGATA AC CCCCTAT TG	STATE CTOGGE STTGCS CTCACT TARCES GAGTGA SCGGG AGAGGG SCCCC TCTCCG TTCGGC TGCGGC SAGCCG ACAGCA SCCAG ACAGAA SCGTCC TTTCTT	TTOGTAT COOGCTT COOGCTT COOGCTAT COOGCTAT COOGCTAT COOGCTAT COOCCTAT COOCCT	TTCACAT TCCAGTC AGGTCAG TATTGGG ATAACCC TCAGCTC AGTCGAG CAAAAGG GTTTTCC	TTCGGAC GGGAAAC CCCITTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT
	6161 6231	TTTAACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTC GAGCGAG ATACGCT TATGCCA	ATAGGCG TGAGCTA CTCGAT GCATTAA CGTAATT ACTGACT TGACTGA TTATCCAC ATAGGTG	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG GCGACGC AGAATCA TCTTAGT	AGGTGTG TT TTAATTG CG AATTAAC GG GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GGGGATA AC CCCTAT TG TGCTGGC GT	GTATE CTCGGC STTEGC CTCACT NACGC GAGGG GAGGGG GAGGGC TCCCG TCTCCG TCGGC TGCGGC NAGCCG ACACCG SCCACG AAACT TTTTTC CATAGG	TTOGTAT TOGGET GGGCGAR GTTTGCG CAAACGC AGCGCAT TCGCCAT TACACTC TCGCCCC	TTCACAT TCCAGTC AGGTCAG TATTGGG ATAACCC TCAGCTC AGTCGAG CAAAAGG GTTTTCC	TTCGGAC GGGAAAC CCCITTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT ACAAAAA
50	6161 6231 6301 6371	TTTAACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTC GAGCGAG ATACGGT TATGCCA GGAACCG	ATAGGCG TGAGCIA ACTCGAT GCATTAA CGTAATT ACTGACT TGACTGA TATCCAC ATAGGTG TAAAAAG	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG GCGACGC AGAATCA TCTTAGT GCCGCGT	AGGTGTG TT TTAATTG CG AATTAAC GG GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GGGGATA AC CCCCTAT TG TGCTGCC CA	TTATE CTOSEC TTATE CTOACT TARGE GAGTGA TGGGG AGAGGC TCCGG TCGGG AGGCC TAGGC AGGCG AGCCG TCTCGG TCGGG TAGGCG ACGCGG ACGCGG TCTTTCTT TCTTTC CATAGAA TABABAG GTATCC	C TTOSTAT CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTAGCC TCAGCTC AGTCGAG CAAAAAGG GTTTTCC CCCTGAC	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGCAT CCGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT
	6161 6231 6301	TTTAACA TAATGAG ATTACTO GCCAGCT CGGTCGA CTCGCTC GAGCGAG ATACGGT TATGCCA GGAACCG CCTTGGC	ATAGGCG TGAGCTA ACTCGAT GCATTAA CGTAATT CGTAATT TGACTGA TTATCCAC ATAGGTG TATAANAG TATTTTTC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG GCGACGC AGAATCA TCTTAGT GCCGCGT AGAGGTGCA	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG GC GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG CG GCGAAAC CC	TTATE CTCGEC TTATE CTCACT TARGEC GAGTGA TGGGEG AGAGGC TCGGEC TCTCGG TCGGEC AGAGGA TAGGCC ACCCCG TCTCAG AAAAAA TCTTTC CATAGG TTATACC TAAAAG GACTAT	TTCSTAI CCGCCTI CGGCGAA GGGGGAA GGGGGGAA CGGGGGAA CGGGGGAA CGGGGGAA CGGGGGAA CGGGGGAA CGGGGGGAA AAGATAC	TTCACAT TCCAGTC AGGTCAG TATTGGG ATANCCC TCAGCTC AGTCGAG CAAAAGG GTTTTCC CCCTGAC GGGACTG	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC
50	6161 6231 6301 6371 6441	TTTAACA TAATGAG ATTACTO GCCAGCT CGGTCGA GCGAGCAG ATACGGT TATGCCA GGAACCG CCTTGGC TCGACGC	ATAGGCG TGAGCTA ACTCGAT ACTCGAT GCATTAA CGTAATT ACTGACT TGACTGA TATCCAC ATAGGTG TAAAAAG ATTTTTC ACTGAGTC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGACGC AGAATCA TCTTAGT GCCGCGT CGGCGCA AGAGGTG	AGGTGTG TT TTAATTG CG AATTAAC GG GCCAACG CG CGGTTGC GC CGGTTGC GT GAGCCAG CA CCCCTAT TG TGCTGGC GT ACGACCG CA GCGAAAC CC CGCTTTTG GG	TTATE CTCGGC STTGCC CTCATC STAGCC GAGTGA SIGGGG AGAGGC STCGGC TCTCGG STGGGC ACAGCC SCAGG AAAGAA SIGGTCC TTTCTT TTTTC CATAGG SAAAAG GATATC SCAGG GATATT SCTGTC CTGATA	TTCSTAI CCCCCTI CCCCCTI CCCCCTI CCCCCCI CCCCCCI CCCCCCI CCCCCCCC	TTCACAT TCCAGTC AGGTCAG TATTGGG ATTACCC TCAGCTC AGTCGAG CABAAGG CABAAGG CCTGAC CGGGACTG CGGGACTG CAGGGGT CGGCAGGGGT GTCCGCA	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC TCCTCGTAG TTCCCCC AAGGGGG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG
50	6161 6231 6301 6371	TITIACA TAATGAG ATTACTIC GCCAGCT CCGCTCGA CTCGCTC GAGCGAG ATACGGT TATGCCA GGAACCG CCTTGGC TCGACGC	ATAGGCG TGAGCTA ACTCGAT CGTAATT ACTGACT TGACTGA TATACCAC TATAGGTG TANAAAG ATTTTTC TCAAGTC AGTCAAGTC AGTCAAGTC AGTCAAGTC AGTCAAGTC AGTCAAGTC AGTCAAGTC AGTCAAGTC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	AGGTGTG TT TTAATTG GC AATTHAC GC GCCAACG CG CGGTTGC GC CTCGGTC GC GGGGATA AC CCCCTAT TG TGCTGGC CA GCGAAAC CC GCGAAAC CC	ETATE CTOSEC ETTAGE CTCACT PAGGE AGAGG AGAGG TTCGG TGGGG AGAGAA AGAA AGA	TTOSTAI COGCTI C	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG TCAGCTC TCAGCTC AGTCGAG CAAAAGG GTTTTCC CCCTGAC GGGACTG CAGGCGT CAGGCGT CAGGCGT CAGGCGT CAGCCGT CCCCCAC CCCCCCTCAC CCCCCCCCCC	TTCGGAC GGGARAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGTA CCGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGGAA
50	6161 6231 6301 6371 6441 6511	TTTAACA TAATGAG ATTACTC GCCAGCT CCGCTCGAGCGAG ATACGGT TATGCCA GGAACCG CCTTGGC TCGACGG AGCTGCG AGCTGCG AGCTGCG AGCTGCG	ATAGGCG TGAGCTA ACTCGAT CGTAATT ACTGACT TGACTGA TTACCAC ATAGGTG TAAAAAG ATTTTCC TCAAGTC AGTCAG AGTCAG AGTCAG AGTCAG AGTCAG AGTCAG AGTCAG AGTCAG AGTCAG	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	AGGTGTG TT TTAATTG GG AATTHAC GG GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GCGGATA AC CCCCTAT TG TGCTGGC GC ACGGCCG CA GCGAAAC CC CGCTTTG GG CCGACCC GC CGGCTGGG AC	TTATE CTCSEC TTATE CTCACT TARCEC GAGTGA GGGGG AGAGGC TTCGGC TGCGG AGAGCA AGAGCA TTCGGC ACGCGG ACAGCA TTTTTC CATAGA AAAAA GGTATC TATATC	TITOTIAI COGCIT	TTCACAT TCCAGTC TCCAGTC AGGTCAG TATTGGG TATTGGG TCAGCTC AGTCGAG CAAAAGG GTTTTCC CCCTGAC GGGGACTG GGCGCTT AGGCCGTA	TTCGGAC GGGARAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA AGGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTT TGGAAGC ACCTTCG TCGGGAA AGGCCTT
50	6161 6231 6301 6371 6441	TTTAACA TAATGAG ATTACTC GCCAGCT GCCAGCT GAGCGAG ATACGGT TATGCCA GGAACCG CCTTGGC TCGACGC AGCTGCG AGCTGCG AGCTGCG AGCTGCG	ATAGGCG TEAGCTA TEAGCTA GCATTAA CGTAATT ACTGACT TACCAC ATAGGTG ATATTTTC TCAAGTC AGTCAG AGGCAG AGCGAG AGCTAGT AGGCAG AGCGAG AGCTAGT AGGCAG AGCGAG AGCTAGCAG AGGCAGAG AGCGAG AGCTAGCAG AGCGAG AGCTAGCAG AGCGAG AGCTAGCAG AGCTAGCAG AGCTAGCAG AGCTAGCAG AGCGAG AGCTAGCAG AGCTAGCAG AGCTAGCAG AGCGAG AGCTAGCAG AGCGAG AGCTAGCAG AG	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG AGAATCA TCTTAGT GCCGCGT CGGCGCA AGAGGTG TCTCCAC TCCTGTT AGGACAA CATAGCT	AGGTGTG TT TTAATTG GG GCCAACG CG GGCTACG GC GGGTTGC GC GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG GT ACGACCG CC CGCTTTG GG CGGACCC TG CGGACCC TG CGGACCC TG CGGACCC TG CGCTGGG TA	TTATE CTOSES TITAGE CTCACT TAACGE GAGTGA TIGGGG AGAGGC TCGGG TGCGG TCGGG AGAGGA TCGGG AGAGGA TCGGG AGAGGA TTTTT CATAGG TAACAG GACTAT TTTTC CTGATA TCGGC TACCGG TACCG TACCGG TACCG TACCGG TACCGG TACCGG TACCGG TACCGG TACCGG TACCGG TACCGG TACCGG	TITOSTAI COGCTI COGCTI COGCGGTA COGGGTA COGGGTA COGGGTA COGGGTA COGGGGGGGA COGGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGA COGGGGGGA COGGGGGGGA COGGGGGGGA COGGGGGGGGA COGGGGGGGGGG	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG TATTGGG CANAAGG CANAAGG GTTTTCC CCCTGAC CGGGGAA GGGGGGAA GGGCGTA	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA ACTCAAA GGTCGTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGCAA AGCCCTT AGCTGGCA
50	6161 6231 6301 6371 6441 6511	TITTACA TAATGAG GCCAGCT GGCAGCT GGGCAGCA ATACGGT TATGCCA GGAACCG TCGACGG AGCTGGG AGCTGGG AGCTGGG GCGTGGG GCGCACCG	ATAGGCG TGAGCTA GCATTAA CGTAATT GCATTAA TGACTGA TATCCAC ATAGGTG TATAAAAG TCAAGTC AGTTCAG AGGAGAG AGGAAGAA AGAAGAAC AGAAGAAC AGAAGAAC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGACGC AGAATCA TCTTAGT GCGCGGT TCTCCAC TCTCCAC TCTCCAC TCTCGTTT TGGACAC AGAGGTG TCTCCAC TCTGTTT AGGACAA CATAGCT	AGGTGTG TT TTAATTG CG AATTHAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GGGGATA AC CCCCTAT TG TGCTGGC CA GCGAACC CA GCGAACC CC GCTTTG GG CCGACCC TG GCGCCC TG GCCTGGG AC CACGCTG TA TCAGCCC GA TCACGCTG TA TCAGCCC GA TTCAGCCC GA TTCAGCCC GA TTCAGCCC GA TTCAGCCC GA	ETATE CTOSEC ETTAGE CTCACT PARCEC GAGTGA AGAGG AGAGGC TCOGG AGAGA AGAGA AGAGA AGAGA GATTAT CATAGG ATAGA AGAGA ATGCCATA GAGTCA AGAGTA	C TICGIAI C COGCTI C GGGGAA GG GTITGCG C CAAACGC C TCGCCAI C TCGCCAI C ATGTGAG AAGATAC T TICIATC T TTCIATC T ATGGAC T AT	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTACCC AGTCGAG CAAAAGG CAAAAGG CAAGCTC CAGGACTG CAGGACTG GGGACTG GGCGCTT AGCCGAA AGCCGTT AGCCGAA AGCCGTT	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA GGCGAGGT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TGGAAGC ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG TCGGCAAC AGCTGGG TCGACCC GTCCAAC
50	6161 6231 6301 6371 6441 6511	TTTAACA TAATGAG ATTACTC GCCAGCT GGCAGCT GAGCGAG ATACGGT TATGCCA GGAACCG CTGGGC TCGACGG AGCTGGG GCGTGGG GCGTGGG CCTGGGC AGCTGGG CCTGGGC CCTGGGC CCTGGGC CCTGGGC CCTGGGC CCTGGGC CCTGGGC CGCACGG CCTGGGC CCTGTGGG	ATAGGCG TGAGCTA TGAGCTA CGTAATT CGTAATT ACTGACT ATAGGTG ATAGGTG ATAGGTG ATAGGTG ATAGGTG ATAGGTG ATAGGTG AGTTCAG GGTTCAG GGTTCT CGAAAGA CACGAAG CACGAAG	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCGCA AGAATCA TCTTAGT TCTTAGT TCTTAGT TCTCAC TCTCCAC TCTCGCT TCCTGTT TCTCAC TCTGTAGT TCTCCAC TCCTGTT CCTGTT CCTGTT CCTGTT CCTGTT CCTGTT CCTGTT CCTGTG	AGGTGTG TT TTAATTG GG AATTHAC GG GCCAACG CG GGGTTGC GG CTCGGTC GT GGGCCAG CA GGGGATA AC CCCCTAT TG TGCTGGC GC GCGACAC CC GGCTTTG GG CCGACCC TA GGGCTGGG AC CACGCTG TA GTGCGCA AT TCAGCCC GA ACTCGGCAC AT TCAGCCC GA ACTCGGCAC AT TCAGCCC GA ACTCGGCAC AT TCAGCCC GA ACTCGGCAC CT	TTATE CTOSEC TTATE TTATE CTOACT TARGE GATTAN TO TECHNOLOGY TO TECHNOLOGY TO TECHNOLOGY TO THE TECHNOLO	TROTTAI TOTAI TOTA	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTATACCC AGTTGAG CAAAAGG GTTTTCC GGGGAACTG GGGCACT AGGCGCA GGGCGAA AGGCGAA AGGCGAACACACACA	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA ACTCAAA CGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA GCGAGGT CGCTCCA CGCAGGT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA AGGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGCAA AGCCCTT AGCTGGC TCGACCC GTCCAAC CAGGTTG
50	6161 6231 6301 6371 6441 6511	TTTAACA TAATGAG ATTACTG GCCAGCT GCCAGCT GAGCGAG TATGCCA GGAACCG CCTTGGC TCCCTCG AGGGAGC CGCACCG CGCACCG CGCACCG CCTGTGTG GACCACAC	ATAGGCG TEAGCTA TEAGCTA GCATTAA CGTAATT ACTGACT TACCAC ATAGGTG TATACTAC TAT	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCGCCA TCTTAGT GCGCGCA TCTCAC TCTCAC TCCTGTT AGGACAA GCAGCCG GTATCGA GCACCCGT GTATCGA CCCCGT GGGGCCA CCCCGT GGGGCCA CCCCCGT GGGGCCA CCCCCGT CCCCCGT CCCCCGT CCCCCGT CCCCCGT CCCCCGT CCCCCGT CCCCCTTATCCC	AGGTGTG TT TTAATTG GG GCCAACG CG GGCTTGC GC CGGTTGC GC GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG GA CCGCTTTG GG CCGACCC TG GGGCACC TG GGCTGGG AC CACGCTGG TA GTGCGAC AT TCAGCCC GA AGTCGGC GA AGTCGGC CA	TTATE CTOSES TTATE CTOACT TAGE CTOACT TAGE CAGTEA THE COACT THE CAGTEA THE CA	TITOSTAI COGCTI COGCTI COGCGGTA COGGGTA COGGGTA COGGGTA COGGGTA COGGGGTA COGGGGTA COGGGGGA COGGGGA COGGGGA COGGGGA COGGGGA COGGGA COGGGGA COGGGA COGGGGA COGGGGA COGGGGA COGGGA COGGA COGGGA COGGA COGGGA COGGA COGGGA COGGA C	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG ATANCCC TCAGCTC CCATGACTC CCATGAC GGGACTG GGGGAA GGTCGCA GGCCTT CGGCGAA AGGTCGTT CCAGCAA AGGTCGTT CCAGCAA TTCATAG	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGG GCGTCCA GCGAGGT GTCTTCC CGCTAG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCCGTA AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGCAA AGCCCTT AGCTGGCA TCGCAAC CAGCTTG TCAACC CTCCAAC CAGGTTG
50 55 60	6161 6231 6301 6371 6441 6511 6581	TTTAACA TAATGAG ATTACTC GCCAGCTC GCCAGCTC GAGCGAGC TATGCCA GGAACCG CCTTGGC TCCCTCG AGGGAGC GCGTGGC CCGCACCG CCGCACCG CCGCTAGGC CCGCTAGGC CCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGGC GACACCC CCCGCTAGC GACACCC CCCGCTAGC GACACCC CCCGCTAGC GACACCC CCCGCTACCC CCCGCTACCC CCCGCTACCC CCCCGCTACCC CCCCGCTACCC CCCCCTACCC CCCCCTACCC CCCCCCTACCC CCCCCCTACCC CCCCCTACCC CCCCCTACCC CCCCCTACCC CCCCCCTACCC CCCCCCC CCCCCCCC	ATAGGCG TEAGCTA TEAGCTA CGTAATT CGTAATT ACTGACTA ATAGGTG TAACACA ATAGGTG TAAAAAG TACACCAC ATAGGTG AGTTAA AGTTAAGTCAC ACCACACACACACACACACACACACACACACACAC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCGCGC AGAATCA TCTTAGT GCGCGCA TCTTAGT TCTCAC TCTGTT AGGACAA CATAGCT GTATCGA CCCCGT GGGGCA CCCCGT GGGGCA CCCCGT GGGGCCA CCCCGT GGGGCCA CCCCGT GGGGCCA CCTTATCG	AGGTGTG TT TTAATTG CG AATTAAC GC GCCAACG CG CGCTTGC GC CGGTTGC GT GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG GT ACGACCG TA CGGTTGG GG CCGACCC TG GGCTGGG AC CACGCTG TA GTGCGAC AT TCAGCCC GA AGTCGGG CT CACGCTG TA GTGCGAC AT TCAGCCC GA AGTCGGG CT CCACTGG GC CGCTGGG CT AGTCGGG CT CGGTGGAC GT AGTCGGG CT CGGTGGAC GT AGTCGGG CT CGGTGACC GT	TTATE CTCGEC TTTGCS CTCACT TTAGCS CTCACT TAGGGG AGAGGC TCGGG TGCGGG TCGGG AGAGAA AGAGA TTTTTC CATAGG AAAAAA TTTTTC CATAGG AAAAAA TCGCT TACCGG TACCG TACCGG TACCG TACCGG TACCGG TACCGG TACCG	TITOSTAI COGCTI COGCTI COGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG ATANCCC TCAGCTC CANANAGG TTGATAG TTAGCAG ANTGGTC	TTCGGAC GGGAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCT AAGGGGG TCTCCCT AGAGGGA GGCATCCCT AGAGGGA GCCAGGT GCGAGGT GCGAGGT GCGAGGT GCGAGGT TCCCTCA GCGAGCT GCGAGCT AGCGAGGT TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCA TCCCTCCA TCCCTCCA TCCCTCC	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGTA AAGGCCA TTCCGGT ACAAAAA TGTTTT TGGAAGC ACCTTCG TCGGAA AGCCCT AGCCCGT CGACCC GTCCAAC CAGGTTG TATGTAG ATACATC
50	6161 6231 6301 6371 6441 6511 6581	TITTACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTCC GAGCGAG ATACGGT TATGCCA GCATCGC TCGACCG AGCTGCG AGCTGCG AGCTGCG AGCTGCG AGCTGCG CGCACCG CCGCTAG CCGGTAA	ATAGGGG TGAGCTA GCATTAA CGTAATT ACTGACT TGACTGA TATCCAC ATAGGTG TATAAAAG TCAGTCAC AGTTCAG AGTTCAG AGTTCAG AGTTCAG GCTTTCT CGAAAGA GCTTTCT CGAAAGA CGTGTTCT GGACGAG CGTGTTCT GACACGAC CTGTGCT TACAGGAC TACAGAAC TAC	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGACGC AGAATCA TCTTAGT GCGCGCT TCTCCAC TCTCCAC TCTCCAC TCTCGTT TGGACCA AGAGTG TCTCCAC TCCTGTT GGACCA CATAGCT GTATCGA CATAGCT GGGGGCA CTTATCG GAATAGCT TCTTTGA	AGGTGTG TT TTAATTG CG AATTHAC GC GCCAACG CG CGGTTGC GC CTCGGTC GT GAGCCAG CA GGGATA AC CCCCTAT TG TGCTGGC CA GCGAACC CA GCGAACC CG CCGACCC GG CCGACCC TA GTGCGCA AC CACGCTG TA CTCAGCCC GC CACGCTG TA CTCAGCCC CA CTCACTGG CA	TATATE CTOSSES TATAGE CTCACT TARGEG GAGTGA TCGGGG AGAGGG TCGGGG AGAGGA TCGGGG AGAGAA AGAGA AGAGAA AG	TITOSTAI COCCOTT COCCO	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTATACCC AGTGAG CABAAGG CABAAGG CAGGACTG CAGGACTG AGGCCTT AGGCGAA AGGCGTT AGGCGAA TTGATAG TTGATAG AATTGATCG AAGGACA AGGACA	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA GCCAGGT CTCTTGA CAGAACT AGCGAGG CTCTTGA CAGAACT AGCGAGGG CGCTCCA GCGAGGT CGCTCC CGGAGGT CGGTCC CGGTCT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TCGGACC ACCTTCG GTCCACC CAGGTTG CTGTCACC CAGGTTG TATGTAG ATACATC GTATCTG
50 55 60	6161 6231 6301 6371 6441 6511 6581 6651 6721	TTTAACA TAATGAG ATTACTC GCCAGCT GGCAGCT GAGCGAG ATACGGT TATGCCA GGAACCG CTGAGGC TCCCTCG AGGAGG GCGTGGG CCTGTGGC CTGTGGC CCTGTGGC CCTGTGGC CCGCACGG CCGCACGG CCGCACGG CCGCACGG CCGCACGG CCGCTGGC CCGGTGGC CCGGGGC CCGGGC CCGGGGC CCGGGGC CCGGGGC CCGGGGC CCGGGGC CCGGGGC CCGGGGC CCGGGCGC CCGGGCGC CCGGGCGC CCGGGCGC CCGGGCGC CCGGGCGC CCGGGCGC CCGGCGC CCGGGCGC CCGGCGCGC CCGGCGCGC CCGGCGCGC CCGGCGCGC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCGCC CCGGCCC CCGGCCC CCGGCCCCC CCGCGCCC CCGCCCCCC	ATAGGCG TGAGCTA GCATTAA CGTAATT CGTAATT ACTGACT ATAGGTG ATAGGTG ATAGGTG ATAGGTG ATATTTCC TCAAGTC AGCGCAG GCTTTCT CGAAAGA CACGAAG CACGAAC GGACGAC GACACCA ATAGGCCT CTACACCA ATAGGTC AGCTC AGCTC AGCTC AGCTC AGCTC AGCAAC AGCAAC AGCAAC AGCAAC AGCAAC AGCAC AG	AGTGTTA ACTCACA TCACAG ACTTAGC GCGCGCA AGAATCA TCTTAGT TCTCAC TCTCCAC TCTCCAC TCTCGCT TCCCGCT AGGACAC AGAGGTG TCTCCAC TCCTGTT CGGCGCA CATAGCT GTATCGA CTTATCG GCGGGCA CCTTATCG GAATAGC TCTTTACAC TCTTTACAC TCTTTACAC TCTTTACAC TCTTTACAC TCTTTACAC TCTTTACAC TCTTTACAC TTCTTGA	AGGTGTG TT TTAATTG GG AATTHAC GG GCCAACG CG GGGTTGC GG CTCGGTC GT GGGCCAG CA GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCC CA GCGAAAC CC CGCTTTG GG CCACCCT TA GTGCGGC AC CACGCTG TA GTGCGGC CA GCGACCC TA CTACCCCC GC CCACTGG CA CTACGCCC GT AGTGGGC CA GTGACCC GT AGTGGTG CA GTGACCC GT AGTGGTG CA CCACTGG CA GTGACCC GT ACTGGTG CA CCACTGC CA CTCACCAC CC	TTATE CTOSEC STATES CTOACT STA	TITOTIAI COGCOTI COGCO	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTACAG CAAAAGG CAAAAGG CAGGCTT CAGGCTC CAGGCTT CAGGCTA GGCGCTA CAGGCTA CAGGCTA CAGGCTA CAGCAA AGTCGTA TTAGCAG TTAGCAG AAAGGACA AAAGGACA TTCCAGCAC TTAGCAG TTAGCAG TTAGCAG TTAGCAG	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA ACTCAAA ACTCAAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA GCGAGGT CTCTTGA CGCTCCA GCGAGGT TCTCTTAG CTCTTTGA CTCTTTGA CTCTTTGA CTCTTTGA CTCTTTGA CTCTTCCCT CTTTTTTG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA AGGCCAT AAGGCCAT ACAAAAA TGTTTTT TGGAAGC ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG TCGGCAC CTCCACC CTCCACC CTCCATC ATTCTAG ATACATC CTATCTC CTATCTC CTATCTC
50 55 60	6161 6231 6301 6371 6441 6511 6581 6651	TTTAACA TAATGAG ATTACTC GCCAGCT GCCAGCT GAGCGAG TATGCCA GGAACCG CCTTGGC TCCCTCG AGGAGCG GCCACCG CCTGTGGC CCCACCG GCACCG CCGCTAGGC CCCCCTTGGC CCCCCCC CCGTAA	ATAGGCG TEAGCTA TEAGCTA GCATTAA CGTAATT CGTAATT ACTGACT ATAGGTG TATACAC ATAGGTG TATATTTTC TCAGGCG GTGCTCAG CAGGAGA CAGGAAGA CAGGAAG CAGGAAGA CTGTGCT TACAGAG CAGGAAGA CTGTGCT TACAGAG CTGTGCT CTGTAGCC CTGTGCT CTGTAGCC CTGTTGCT CTGTAGCC CTGTACAC CTGTAGCC CTGTAGC CTGT	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG AGAATCA TCTTAGT GCCGCGT AGAGGTG TCTCAC TCCTGTT AGGACAA CATAGCT GTATCGA CTTATCG CCCCGT GGGGCA CTTATCG GAATAGC TCTTGAA AGAGTG CTTCTTAA	AGGTGTG TT TTAATTG GG GCCAACG CG GGCTAC GC GGGTTGC GC GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG GA ACGACCG TG GGGATA CC CGCTTTG GG CCACCTGGT TG GTGCGC TA GTGCGC GA AGTCGGG CA AGTCGGG CA CCACTGGG CA CCACTGGG CA CTCACCAC GT AGTGGTG GC CCACTGG CA CCTCTGGA AA CCCCTTGGA CA CCTCTGGA AA CTTCGGA AA	TTATE CTOSES TTATE CTOSES TTATES CTOACT PARCEC GRATGA DEGGE AGREGE TTOGGE TOTOGG TTOGGE AGREGE TOGGE AGREGE TOGGE AGREGE TOGGE AGREGE TOTTTT CATRAGE AGRACAC GACTAT TOTTT CATRAGE TACCAGE AGREGE TACCAGE TACCA	TITOTIAI COGCTI COGCTI COGCTI COGCGGAACGC COAACGC COACGC CO	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG ATANCCC TCAGCTC CCAGACG CCAGACG GGGACTG GGGCAT CCAGCCTT CCAGCCAT CCAGCCAT CCAGCAA AGGTCGTT CCAGCAA AGGTCGTT CCAGCAA ATTGATAG ATTACAG ATTGATAG ATTGATAG ATTGATAG ATTGATAG ATTCCTGT ATCCGGT ATCCGGCA	TTCGGAC GGGAAAC CCCTTTG GGGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA GCAAGGT GTCTTCC GCAAGT TTCCCCC AAGGGGA CGCTCCA GCAAGT GTCTTGA TTCCCCC GCAAGT GTCTTGA TTCCCCC AAGACT AGAACT AGCAACT AGCAACT AGCAAAAAAAAAA	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA AGGCCAT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGCAT AGCCCTTCG TCGCACC TCGCACC GTCCAAC TCGACCC GTCCAAC TATGTTAG TATGTTAG TATGTTAG CATAGAC CACCGCT
50 55 60	6161 6231 6301 6371 6441 6511 6581 6651 6721 6791	TITTAACA TAATGAG GCCAGCT GGCAGCA GAGCAGG ATACGCT TATGCCA GGAACCG TCGACTGG AGCTGGG AGCTGGG CCTTGGC TCGACGC AGCTGGC CCTTGGC CGCACCG GCACCG GCACCG GCCATGG GCCATG	ATAGGGG TGAGCTA ACTGATT CGTAATT TGACTGAT TATCCAC ATAGGTG TATACAC ATAGGTG TATACAC ATAGGTG TATACAC ATAGGTG ATTTTTC ACGCGAG GCTTTCT ACGCGAG CACGAGC CACGAGC CACGAGC TACCGAG CACGAGC CACGA	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG AGAATCA TCTTAGT CCGCGGCA AGAGTTA CCTCCAC TCCTGTT AGGACAA CCATAGCT GTATCGA CCCCCGT GGGGGCA CCTTATCG GGATAGC TCTTTGAATAGC CTCTTTGAATAGC CAGTTAC CAGTTAC CAGTTAC CAGTTAC CAGTTAC	AGGTGTG TT TTAATTG CG AATTHAC GC GCCAACG CG GGGTTGC GC CTCGGTC GC GGGGATA AC CCCCTAT TG TGCTGGC CA GCGAACC CA GCGAACC CG CCGACCC TG GGCTGGG AC CACGCTG TA TCAGCCC GA AGTCGGC CA AGTCGCC CA AGTCCCC AGTCCCC AGTCCC A	TATATE CTCGGC TATAGE CTCACT TAACGC GAGTGA TCGGGG AGAGGG TCGGGG AGAGGA TCGGC TCCGG TCGGG AAAGAA SCGTCC TTCTTC TATATC TATAT	C TROSTAI C TROSTAI C GGGGTAR GGGGTAR GGGGTAR C TROSCCAI C ATOTAR C TROCCCAI C TROCCAI	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTCGAG CANAAGG CANAAGG CANAAGG GGACTG GGGACTG GGGCGTA GGGCGTA AGTCGTA AGTCGTA AACTATC ATTGACAG AATTATC AATGGTC AAGGACA TTCCTGT AAGGACA TCCGGCA AACTATC AATGGTC AAGGACA AGGACA AGGCGT	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA AGAGGGA GTCTTGA CGGAGGT CTCTTGA CGGAGGT CTCTTGA CAGAACT AGCAACT AGCAACT AGCAACT AGCAACT AGCAACT TTGTTTG	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TGGAAGC ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG TCGGGAA AGCCCTT AGCTGGG TCGACCC GTCCAAC CAGGTTG TATGTAG ATACATC GTATCTG CATACAC CACCGCT GTGCCCA GTGCCCAC CACCGCT GTGCCCAC CACCGCT GTGCCCAC CACCGCT GTGCCCCAC CACCGCT GTGCCCCAC CACCGCT GTGCCCCAC CACCGCT GTGCCCCAC GTGCCCCAC CACCGCT GTGCCCCAC CTGCCCCC GTGCCCCAC CTCCCCCT GTGCCCCAC CTGCCCCCT GTGCCCCAC CTGCCCCAC CTGCCCCCT GTGCCCCAC CTGCCCCC GTCCCCCC GTCCCCCCC GTCCCCCC GTCCCCCCC GTCCCCCC GTCCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCC GTCCCCCCCC
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50 55 60	6161 6231 6301 6371 6441 6511 6581 6651 6721 6791 6861	TTTAACA TAATGAG ATTACTC GCCAGCT GCCAGCT GAGCGG ATACGGT TATGCCA GGAACCG CCTTGGC AGCTGGC AGCTGGC AGCTGGC CCCTTGGC CCCCCG GCACCG CCGCACCG CCGCACG CCGCACG CCCACGG CCACGG CCACGC CCACG CCACGG CCACGG CCACGG CCACGG CCACGG CCACGG CCACGG CCACGG CCACGG	ATAGGCG TEAGCTA TEAGCTA CGTATTA CGTAATT CGTAATT ACTGACT ATAGGTG TTACCAC ATAGGTG TTACACC ATAGGTG TCAAGTC ATAGGTG TCAAGTC ATTTTTC CGAAAGA CCACGAAC CTGTGCTT CGAAACA CTGTGCTT CTAAGTC CTGTGCT CTGAAGC CTGTGCT CTGAAGC CTGTGCT CTGAAGC CTGTGCT CTGAAGC CTGTGCT CTACAGAG CTGTGCT CTGAAGC CTGTGCT CTACAGAG CTGTGCT CTACACAA CTGTCT CTACACAA CTGTCT CTACACAA CTGTCT CTACACAA CTGTCT CTACACAA CTGTCT CTACACAA CTCTTC CTACACAA CTTCT CTACA	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC CGCTGCG AGAATCA TCTTAGT GCCGCGT AGAGCGC AGAGCGC AGAGCGC AGAGCGC AGAGCGC TCCTGTT AGGACAA CATAGCT GTATCGA CTTATCG GAGTACC GAATAGC TCTTGAA AGAACT TCTTGAA AGAACT TCTTGAA AGAACT TCTTGAA AGAACT TTTTGTT AAAACAA GGGTCAATGC TTTTTGTT AAAACAA GGGTCTT	AGGTGTG TT TTAATTG GO GCCHACG CG GCCHACG CG CGGTTGC GC CGGTTGC GC GGGGATA AC CCCCTAT TG TGCTGGC GT ACGACCG GA GCGAAAC CC CGCTTTG GG CCACGTGG AC GGCTGGA AC CCACGTG TA GTGCGC GA AGTCGG CA GGTGGG CA AGTCGG CA AC CTTCGGA CA ACGTTCG GA ACGTTCG GT	TTATE CTOSEC TTATE CTOSEC TTATES CTOACT TARGE GRATGA TEGGE AGAGGE TCGGE TGCGG TCGGE AGAGAE TCGGE AGAGAE TCGGE AGAGAE TCGGE AGAGCE TCTCT TTTTT CATAGA TACAGA TTCTC TAACAGA TTCTC TAACAGA TTCTC TAACAGA TACAGA	TITOSTAI COGCOTT COGCO	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG ATANCCC TAGGCTC CAGACAG CANAAGG CANAAGG CAGACAG GGCGTA GGCGCTA CAGCAGAA AGGCGTA ATTGATAG ATTAGCAG	TTCGGAC GGGAAAC CCCTTTG CGCTCTT GCGAGAA ACTCAAA ACTCAAA GGTCGTT GAGCATC CTCCTTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGG CGCTCCA GCAAGT CAGAACT AGCAACT AGCAACT AGCAACT TCTTGAACAA ACTTGTTTG TCAAGAA AGTTCTT TTTGGTCA	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA AGGCCAT AAGGCCA TTCCGGT ACAAAAA TGTTTTT TGGAAGC ACCTTCG TCGGCAA AGCCCTTCA AGCTGGCTA AGCTGGG TCGACCC GTCCAAC CAGGTTG TATGTAG ATACATC GTATCTG CATAGAC CACGCT GTGGCGA GATCCTT GTGGCGA CATCGTAGAC CACGCT GTGGCGA TTATCTAGAC CACGCT GTGGCGA GATCCTT TAGGAAT TGAGAAT TGAGAAT
50556065	6161 6231 6301 6371 6441 6511 6581 6651 6721 6791	TITTACA TAATGAG ATTACTO GCCAGCT CGGTCGA CTCGCTCC GAGCGAG ATACGCT TATGCCA GGAACCG TCGACGC AGCTGCG CCTTGGC AGCTGCG CCTGGC CCTGGC AGCTGCC CCGTGGC CGCACCG CCGCTCG GCCACCG CGCACCG CGCACCG CGCACCG CGCACCG CGCTCTGC CGCACGC CCATCGC CCATCGC CCATCGC CCATCGC CATCGC CATCGC CATCGC CCATCGC CCATCGC CCATCGC CATCGC CCATCGC CATCGC CCATCGC CATCGC CAT	ATAGGGG TGAGCTA ACTGACT TGACTGAC TGACTGAC TATACCAC ATAGGTG TACACGAG GCTTTCT ACGCGAG GCTTCT CACACAC GTCCTTG TACACGAG ATGTCTC TACAGAG ATGTCTC GACTTCG AGAGG ATGTCTC ACCAAA	AGTGTTA ACTCACA TGAGTGT TGAATCG ACTTAGC GCGCACGC AGAATCA TCTTAGT GCGCGCA AGAGTGA AGAGTGA AGAGTG TCTCCAC TCTTCCAC CATAGCT GCGCGCA AGAGTGA CATAGCT GCGCGCA CTTATCGA CATAGCT TCTATTAGCT TCTATTAGCT TCTATCATT AGAAACTA CAGTTACCA TCTATTGGT TAGATAGC TTTTTGTT AAAACAA GGGTCTG CCCAGGAC CCCCAGGAC TCCAGGAC TTTTTGTT AAAACAA	AGGTGTG TT TTAATTG CG AATTHAC GC GCCAACG CG GGGTTGC GC CTCGGTC GT GAGCCAG CA GGGGATA AC CCCCTAT TG ACGACCG CA GCGAAAC CC GCGTTGG GC ACGCTGT TG CCGACCG TG GGCTGGG AC CACGCTG TA GTCGAC AT TCAGCCC GA AGTCGGC CT AGTCGGC CT AGTCGGC CT AGTCGTAC CG ACGCTCA TT TGCAAGC AG ACGTTCG TC ACGCTCA TT TGCAAGC TC ACGCTCA TT TGCAAGC TC ACGCTCA TC ACGCTCA TC TGCAAGC TC ACGCTCA TC TGCAAGC TC ACGCTCA TC ACGCTCA TC TGCAAGC TC ACGCTCA TC ACCCTCA TC	GTATG CTCGGC STTAGG CTCACT PAACGC GAGTGA GGGGG AGAGGG AGCCC TCTCGG TCGGG ACGCGG AGAGA AGAGA AGGCG ACGCGG AGAGA AGAGA AGGTC TTTCTTC CATAGG AAAAAG GTATCC CTGATA AGCGGT TACCGG AGGGA ATGCC AGGTAT CCATA AGCGCT GCGCCT TGCGAC GCGCA AGGGA ATGCC AGGTAT CTCAGT TCCATA GAGTCA AGCGCT GCGCCT TGGGCG AGCCGC AGGTAT ATGCGG CTTACC CTGAGC CACTGG AGAGAC CACTGG CAGAGA AGAGAC CAGGAC CAGCAC CAGGAC CAGC CAGGAC CAGGAC CAGGAC CAGGAC CAGGAC CAGCAC CAGCAC CAGGAC CAGGA	C TICGTAI C TICGTAI C GGGGIAA GG GTTTGCG C CAAACGC C CAACGC C ATGTGAG C TCGCCCA G AGGCGGA AAGATAG A TACCTGT A TACCGGT A TAGGCCA A TAGGCCA C GAGAACA C GAGAACA C GAGAACA C GAGAACA C GAGAACA C GAGAACA A TGTGTTTT C CACGTTT A CGCGTAT A GGCGAACT C GAGAACA A GGGCAAA A TGTGTAT C GAGAACA C GAGAACA C GAGAACA A GGGCAAT C CACGTTT A CACGTTA A GGGCAAT	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG TATTGGG CANAAGG CANAAGG GGTATTTCC GGGACTG GGGACTG GGGCGTA GGGCGTA GGCGGAA AGTCGTA AGTCGTA AACTATC TTGATAG AATGTC AATGGTC AAGGACA TTCCTGT AGGGACT TTCCTGT AGGGACT TTCCTGT AGGGACT AGGGACT TTCCTGT AGGGACT TTCCTAG	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTT GAGCATC CTCGTAG TTCCCCC AAGGGGG TCTCCCT AGAGGGA CGCTCCA AGCGAGGT GTCTTGA CAGAACT AGCAGG GTCTTGA CAGAACT TTGACAGAA ACTAAAC AACAAAC TTCAAGAA AGTTCTT TCAAGAA AGTTCTT TTCGTCA AACCAGT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCGATG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TCGGAGC ACCTTCG ACCATCA ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG ACCTTCG TCGGCAA AGCCCTT AGCTGGACC CAGGTTG TATGTAG ATACATC GTATCTG CATAGAC CACCGCT GTGGCCA GATCCTT CTAGGAA TGAGATT ACTCTAA
50556065	6161 6231 6301 6371 6441 6511 6581 6651 6721 6791 6861 6931	TITTACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTCC GAGCGAG ATACGGT TATGCCA GGAACCG TCGACGC AGCTGGC AGCTGGC AGCTGGC AGCTGGC AGCTGGC AGCTGCC CGCACG CGCACG CGCACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CCATTGGC ACTAGGAA ATCAAAA	ATAGGGG TGAGCTA TGAGTTA CGTAATT CGTAATT TGACTGA TATCCAC ATAGGTG TATACAC ATAGGTG TATACAC ATAGGTG TATACAC AGGTCAC AGGTCAC AGGTCAC AGGTCAC AGGTCAC AGGAGC CGTGTTCT AGGATCC AGGAGC CTGTGCT CTGAAGAC CTGTACT CTGAAGC CTGAAGC CTGTACC CTGAAGC CTGAACC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAACC CTGAAGC CTGAACC CTGAAGC CTGAACC CTGAAC	AGTGTTA ACTCACA TCACTAGC TGAATCG ACTTAGC GCGACGC AGAATCA TCTTAGT TCGGCGCA AGAGGTG TCTCCAC TCTCGTT TCTCCAC TCTTAGT GGGGGCA AGAGGTG TCTCCAC TCTTATCG GTATCGA CATAGCT GTATCGA CTTATCG GAATAGC TTCTTAG TTCTTGA TTCTTAG TTCTTAG TTCTTAG TTCTTAG TTCTTTGTT TTTTGTT TTTTGTT TANAACAA GGGTCTG CCCAGACC	AGGTGTG TT TTAATTG GO GCCAACG CG GGCTTGC GC CTCGGTC GT GGGCCAC CA GGGGATA AC CCCCTAT TG TGCTGGC GT GCGACCC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGCTG GA CCGCTGG CC CCGCTG GA CCACTGG CA CTCACCAC CG CTTCGGA AA GAGCCT TT TGCAAGC CG TGCCACTG GA ACGTTCG TC ACGCTCA GT TGCGAGT TA ACGCTCA GT TGCGAGT TA ACGCTCA GT TGCGAGT TT TGCAACC TT ACGCTCA GT TGCGAGT TT	GTATE CTOSEC STATES CTOACT STAGE CACACT TOCACT TOCA	C TICGIAI C GGGGIAA GG GTTTGCG GGGGIAA C TAGGCG ATGTGAG AAGATAG TTCTCATC ATGGAC TTCTCTT ATGGAC TTCTCTT ATGGAC TTCTCTT ATGGAC TTCTCTT ACACTAG ATGGAAC TTCTCTT C GAGAACA TCTTTT C AGAACA TCTTTT C AGAACA TCTTTT T ACACTTAG ATGTGAT ATGGAACT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA AGGGAACA AGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGAACA AGGA	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTTTCC AGGTCAG CABAAGG CABAAGG CABAAGG CAGGAA GGCGTA GGCGCTA GGCGCAA AGGTCGTA AACTATC AATCGTC AAGGACA TTCCTGT AGGCGCAA AGGCCTT AGGCGCAA AGGCCTT AGGCCTT AGGCCACAA AGGCCTT AGGCCACAAA AGGCCTT AGGCCACAAA AGGCCTT AGGCCTT AGGCCACAAA AACTCACC AAGGACA	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTTT GAGCATC TTCCCCC AGAGGGG TCTCCTA GGTCTCC AGAGGGA CGCTCCA GCGAGGT TCTCAAA CTTGTTG CATAAAC AACAAAC TTGTTTG TCAAGAA AGTTCTT TTGGTCA AACCAGT AACCAGT TCAAAAC AACCAGT TTCAAAGAA AGTTCTT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TGGAAGC ACCATTCT TGGAAGC ACCTTCG TCGGCAA AGCCCTT AGCTGGA AGCCCTT AGCTGGA TCGACCC CAGCTTG TATGTAG ATACATC CATAGAC CACCGCT GTAGAC CACCGCT GTAGAC CACCGCT GTAGAC CATCGTAGAC CATCGTAGAC CACCGT CTAGAA TGAACTTCTAAA TGAACTTTAATTAT
50556065	6161 6231 6301 6371 6441 6511 6581 6651 6721 6791 6861	TITTACA TAATGAG ATTACTC GCCAGCT CGGTCGA CTCGCTCC GAGCGAG ATACGGT TATGCCA GGAACCG TCGACGC AGCTGGC AGCTGGC AGCTGGC AGCTGGC AGCTGGC AGCTGCC CGCACG CGCACG CGCACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CGCTACG CCATTGGC ACTAGGAA ATCAAAA	ATAGGGG TGAGCTA TGAGTTA CGTAATT CGTAATT TGACTGA TATCCAC ATAGGTG TATACAC ATAGGTG TATACAC ATAGGTG TATACAC AGGTCAC AGGTCAC AGGTCAC AGGTCAC AGGTCAC AGGAGC CGTGTTCT AGGATCC AGGAGC CTGTGCT CTGAAGAC CTGTACT CTGAAGC CTGAAGC CTGTACC CTGAAGC CTGAACC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAAGC CTGAACC CTGAAGC CTGAACC CTGAAGC CTGAACC CTGAAC	AGTGTTA ACTCACA TCACTAGC TGAATCG ACTTAGC GCGACGC AGAATCA TCTTAGT TCGGCGCA AGAGGTG TCTCCAC TCTCGTT TCTCCAC TCTTAGT GGGGGCA AGAGGTG TCTCCAC TCTTATCG GTATCGA CATAGCT GTATCGA CTTATCG GAATAGC TTCTTAG TTCTTGA TTCTTAG TTCTTAG TTCTTAG TTCTTAG TTCTTTGTT TTTTGTT TTTTGTT TANAACAA GGGTCTG CCCAGACC	AGGTGTG TT TTAATTG GO GCCAACG CG GGCTTGC GC CTCGGTC GT GGGCCAC CA GGGGATA AC CCCCTAT TG TGCTGGC GT GCGACCC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGACC GG CCGCTG GA CCGCTGG CC CCGCTG GA CCACTGG CA CTCACCAC CG CTTCGGA AA GAGCCT TT TGCAAGC CG TGCCACTG GA ACGTTCG TC ACGCTCA GT TGCGAGT TA ACGCTCA GT TGCGAGT TA ACGCTCA GT TGCGAGT TT TGCAACC TT ACGCTCA GT TGCGAGT TT	TTATE CTOSEC TTATE CTOSEC TTATES CTOACT TARGE GRATGA TEGGE AGAGGE TCGGE TGCGG TCGGE AGAGAE TCGGE AGAGAE TCGGE AGAGAE TCGGE AGAGCE TCTCT TTTTT CATAGA TACAGA TTCTC TAACAGA TTCTC TAACAGA TTCTC TAACAGA TACAGA	C TICGIAI C GGGGIAA GG GTTTGCG GGGGIAA C TAGGCG ATGTGAG AAGATAG TTCTCATC ATGGAC TTCTCTT ATGGAC TTCTCTT ATGGAC TTCTCTT ATGGAC TTCTCTT ACACTAG ATGGAAC TTCTCTT C GAGAACA TCTTTT C AGAACA TCTTTT C AGAACA TCTTTT T ACACTTAG ATGTGAT ATGGAACT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA ATGTGAT AGAACA AGGGAACA AGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGGAACA AGGAACA AGGA	TTCACAT TCCAGTC AGGTCAG TATTGGG TATTGGG AGTTTCC AGGTCAG CABAAGG CABAAGG CABAAGG CAGGAA GGCGTA GGCGCTA GGCGCAA AGGTCGTA AACTATC AATCGTC AAGGACA TTCCTGT AGGCGCAA AGGCCTT AGGCGCAA AGGCCTT AGGCCTT AGGCCACAA AGGCCTT AGGCCACAAA AGGCCTT AGGCCACAAA AGGCCTT AGGCCTT AGGCCACAAA AACTCACC AAGGACA	TTCGGAC GGGAAAC CCCTTTG GCGAGAA ACTCAAA TGAGTTT CCAGCAA GGTCGTTT GAGCATC TTCCCCC AGAGGGG TCTCCTA GGTCTCC AGAGGGA CGCTCCA GCGAGGT TCTCAAA CTTGTTG CATAAAC AACAAAC TTGTTTG TCAAGAA AGTTCTT TTGGTCA AACCAGT AACCAGT TCAAAAC AACCAGT TTCAAAGAA AGTTCTT	CCCACGG CTGTCGT GACAGCA CCGCTTC GGCCAAG GGCGGTA CCGCCAT AAGGCCA TTCCGGT TCGGTTT TGGAAGC ACCTTCG TCGGCAAA AGCCTTCG TCGGCAAA AGCCTTCG TCGGCAAC CACCGTT TATGTAG ATACATC CATAGAC CACCGCT CATAGAC CACCGCT GTGTAGAC CACCGCT CTAGGAA TGACATC TAGGAA TGAGATT TATATAT

	7141	GAGTAAA CTTGGTC TGACAGT TACCAAT GCTTAAT CAGTGAG GCACCTA TCTCAGC GATCTGT CTATTTC
		CTCATTT GAACCAG ACTGTCA ATGGTTA CGAATTA GTCACTC CGTGGAT AGAGTCG CTAGACA GATAAAG
		Amp resistance gene
5	7211	GTTCATC CATAGIT GCCTGAC TCCCCGT CGTGTAG ATAACTA CGATACG GGAGGGC TTACCAT CTGGCCC
3	/211	CAAGTAG GTATCAA CGGACTG AGGGGCA GCACATC TATTGAT GCTATGC CCTCCCG AATGGTA GACCGGG
		Amo resistance gene
	7281	CAGTECT GCAATGA TACCECE AGACCCA CECTCAC CEECTCC AGATTTA TCAGCAA TAAACCA GCCAGCC
		GTCACGA CGTTACT ATGGCGC TCTGGGT GCGAGTG GCCGAGG TCTAAAT AGTCGTT ATTTGGT CGGTCGG
10		Amp resistance gene
	7351	GGAAGGG CCGAGGG CAGAAGT GGTCCTG CAACTTT ATCCGCC TCCATCC AGTCTAT TAATTGT TGCCGGG
		CCTTCCC GGCTCGC GTCTTCA CCAGGAC GTTGAAA TAGGCGG AGGTAGG TCAGATA ATTAACA ACGGCCC
		Amp resistance gene
	7421	AAGCTAG AGTAAGT AGTTCGC CAGTTAA TAGTTTG CGCAACG TTGTTGC CATTGCT ACAGGCA TCGTGGT
15		TTCGATC TCATTCA TCAAGCG GTCAATT ATCAAAC GCGTTGC AACAACG GTAACGA TGTCCGT AGCACCA
		Amp resistance gene
	7491	GTCACGC TCGTCGT TTGGTAT GGCTTCA TTCAGCT CCGGTTC CCAACGA TCAAGGC GAGTTAC ATGATCC
		CAGTGCG AGCAGCA AACCATA CCGAAGT AAGTCGA GGCCAAG GGTTGCT AGTTCCG CTCAATG TACTAGG
20		Amp resistance gene CCCATGT TGTGCAA AAAAGCG GTTAGCT CCTTCGG TCCTCCG ATCGTTG TCAGAAG TAAGTTG GCCGCAG
20	7561	CCCATGT TGTGCAA AAAAGGG GTTAGCT CCTTCGG TCCTCCG ATCGTTG TCAGAAG TAAGTTG GCCGGTC GGGTACA ACACGTT TTTTCGC CAATCGA GGAAGCC AGGAGGC TAGCAAC AGTCTTC ATTCAAC CGGCGTC
		Amp resistance dene
	7631	TGTTATC ACTUATG GTTATGG CAGCACT GCATAAT TCTCTTA CYGTCAT GCCATCC GTAAGAT GCTTTTC
	7031	ACAATAG TGAGTAC CAATACC GTCGTGA CGTATTA AGAGAAT GACAGTA CGGTAGG CATTCTA CGAAAAG
25		Amp resistance gene
~	7701	TETGACT GETGACT ACTCAC CARGTCA TTCTGAG AATAGTG TATGCGG CGACCGA GTTGCTC TTGCCCG
		ACACTGA CCACTCA TGAGTTG GTTCAGT AAGACTC TTATCAC ATACGCC GCTGGCT CAACGAG AACGGGC
		Amp resistance gene
	7771	GCGTCAA TACGGGA TAATACC GCGCCAC ATAGCAG AACTTTA AAAGTGC TCATCAT TGGAAAA CGTTCTT
30		CGCAGTT ATGCCCT ATTATGG CGCGGTG TATCGTC TTGAAAT TTTCACG AGTAGTA ACCTTTT GCAAGAA
		Amp resistance gene
	7841	CGGGGCG AAAACTC TCAAGGA TCTTACC GCTGTTG AGATCCA GTTCGAT GTAACCC ACTCGTG CACCCAI
		GCCCCGC TTTTGAG AGTTCCT AGAATGG CGACAAC TCTAGGT CAAGCTA CATTGGG TGAGCAC GTGGGTT
		Amp resistance gene CTGATCT TCAGCAT CTTTAC TTTCACC AGCGTT CTGGGTG AGCAAAA ACAGGAA GGCAAAA TGCCGCA
35	7911	CTGATCT TCAGCAT CTTTTAC TITCACC AGCGTT CTGGGTG AGCAMAR ACAGGAR GCCAMAR TCCGGCGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
		Amp resistance gene
	7981	AMA ARGG GARTARG GGCGACA CGGARAT GTTGART ACTCATA CTCTTCC TTTTTCA ATATTAT TGRAGCI
	7981	TITITIC CITATIC COGCIGI GCCITTA CAACITA IGAGIAI GAGAAGG AAAAAGI TATAATA ACITOGI
40		THIRD CHARL COCIET SCALL SANCES.
40		Amo resistance gene
	8051	TITATCA GGGTTAT TGTCTCA TGAGCGG ATACATA TTTGAAT GTATTTA GAAAAAT AAACAAA TAGGGG
		ADATACT CCCAATA ACAGAGT ACTCGCC TATGTAT AAACTTA CATAAAT CTTTTTA TTTGTTT ATCCCC
	8121	TOGGGG ACATTC CCCGAAA AGTGCCA CCTGACG TCTAAGA AACCATT ATTATCA TGACATT AACCTA
45		AGGCGCG TGTAAAG GGGCTTT TCACGGT GGACTGC AGATTCT TTGGTAA TAATAGT ACTGTAA TTGGATA
	8191	AAAATA GGCGTAT CACGAG
		TTTTTAT CCGCATA GTGCTC

FIGURE 2A

	mCEA(6D) mCEA(6D,1st&2nd)	1 ATGGAGTCTC ATGGAGTCTC		TCCCCACAGA TCCCCACAGA		
5	mCEA(6D) mCEA(6D,1st&2nd)			TTCTAACCTT TTCTAACCTT		
10	mCEA(6D) mCEA(6D,1st&2nd)	101 CCAAGCTCAC CCAAGCTCAC	TATTGAATCC TATTGAATCC	ACGCCGTTCA ACGCCGTTCA	ATGTCGCAGA ATGTCGCAGA	150 GGGGAAGGAG GGGGAAGGAG
15	mCEA(6D) mCEA(6D,1st&2nd)			TCTGCCCCAG TCTGCCCCAG		
20	mCEA(6D) mCEA(6D,1st&2nd)			ATGGCAACCG ATGGCAACCG		
	mCEA(6D) mCEA(6D,1st&2nd)			CCAGGGCCCG CCAGGGCCCG		
25	mCEA(6D) mCEA(6D,1st&2nd)	301 ATATACCCCA ATATACCCCA	ATGCATCCCT ATGCATCCCT	GCTGATCCAG GCTGATCCAG	AACATCATCC AACATCATCC	350 AGAATGACAC AGAATGACAC
30	mCEA(6D) mCEA(6D,1st&2nd)	351 AGGATTCTAC AGGATTCTAC	ACCCTACACG ACCCTACACG	TCATAAAGTC TCATAAAGTC	AGATCTTGTG AGATCTTGTG	400 AATGAAGAAG AATGAAGAAG
35	mCEA(6D) mCEA(6D,1st&2nd)			TACCCGGAGC TACCCGGA <u>A</u> C		
40	mCEA(6D) mCEA(6D,1st&2nd)			GGAGGACAAG CGA <u>A</u> GACAA <u>A</u>		
	mCEA(6D) mCEA(6D,1st&2nd)	501 TGAACCTGAG CGAGCCCGAA	ACTCAGGACG ACTCA <u>A</u> GACG	CAACCTACCT CAAC <u>A</u> TA <u>T</u> CT	GTGGTGGGTA CTGGTGGGT <u>G</u>	550 AACAATCAGA AACAA <u>C</u> CAG <u>T</u>
45	mCEA(6D) mCEA(6D,1st&2nd)			CTGCAGCTGT CT <u>C</u> CA <u>A</u> CT <u>CA</u>		
50	mCEA(6D) mCEA(6D,1st&2nd)	601 ACTCTATTCA ACCCTGTT <u>T</u> A	ATGTCACAAG A <u>C</u> GT <u>G</u> AC <u>C</u> AG	AAATGACACA GAACGACACA	GCAAGCTACA GCAAGCTACA	650 AATGTGAAAC AATG <u>C</u> GAAAC

FIGURE 2B

		FIGURE 2B	
e	mCEA(6D) mCEA(6D,1st&2nd)	651 CCAGAACCCA GTGAGTGCCA GGCGCAGTGA TTCAGTCATC CTGAATGT CCAAAATCCA GTCAGCGCCA GGAGGTCTGA TTCAGTGATT CTCAACGT	GC GC 00
5	mCEA(6D) mCEA(6D,1st&2nd)	701 7 TCTATGGCCC GGATGCCCCC ACCATTTCCC CTCTAAACAC ATCTTACA TTTACGGACC CGATGCTCCT ACAATCAGCC CTCTAAACAC AAGCTATA	'50 LGA LGA
10	mCEA(6D) mCEA(6D,1st&2nd)	751 TCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA ACCCACCT TCAGGGGAAA ATCTGAATCT GAGCTGTCAT GCCGCTAGCA ATCCTCCC	100 TGC <u>C</u> GC
15	mCEA(6D) mCEA(6D,1st&2nd)	801 ACAGTACTCT TGGTTTGTCA ATGGGACTTT CCAGCAATCC ACCCAAGA CCAATACAGC TGGTTTGTCA ATGGCACTTT CCAACAGTCC ACCCAGGA	350 AGC A <u>A</u> C
20	mCEA(6D) mCEA(6D,1st&2nd)	851 TCTTTATCCC CAACATCACT GTGAATAATA GTGGATCCTA TACGTGCC TGTTCATTCC CAATATTACC GTGAACAATA GTGGATCCTA CACGTGCC	OO CAA CAA
25	mCEA(6D) mCEA(6D,1st&2nd)	901 GCCCATAACT CAGACACTGG CCTCAATAGG ACCACAGTCA CGACGATG GCTCACAATA GCGACACCGG ACTCAACCGC ACAACCGTGA CGACGATT	950 CAC CAC
20	mCEA(6D) mCEA(6D,1st&2nd)	951 10 AGTCTATGAG CCACCCAAAC CCTTCATCAC CAGCAACAAC TCCAACCC CGTGTATGAG CCACCAAAAC CATTCATAAC TAGTAACAAT TCTAACCC	000 CCG C <u>A</u> G
30	mCEA(6D) mCEA(6D,1st&2nd)	1001 1CGAGGATGA GGATGCTGTA GCCTTAACCT GTGAACCTGA GATTCAGA TTGAGGATGA GGACGCAGTT GCATTAACTT GTGAGCCAGA GATTCAAA	050 AAC AA <u>T</u>
35	mCEA(6D) mCEA(6D,1st&2nd)	1051 12 ACAACCTACC TGTGGTGGGT AAATAATCAG AGCCTCCCGG TCAGTCCC ACCACTTATT TATGGTGGGT CAATAACCAA AGTTTGCCGG TTAGCCCZ	100 CAG ACG
40	mCEA(6D)	1101 11 GCTGCAGCTG TCCAATGACA ACAGGACCCT CACTCTACTC AGTGTCAC CTTGCAGTTG TCTAATGATA ACCGCACATT GACACTCCTG TCCGTTAC	150 CAA CTC
45	mCEA(6D) mCEA(6D,1st&2nd)	1151 12 GGAATGATGT AGGACCCTAT GAGTGTGGAA TCCAGAACGA ATTAAGTC GCAATGATGT AGGACCTTAT GAGTGTGGCA TTCAGAATGA ATTATCCC	200 GTT GTT
40	mCEA(6D) mCEA(6D,1st&2nd)	1201 12 GACCACAGCG ACCCAGTCAT CCTGAATGTC CTCTATGGCC CAGACGAC GATCACTCCG ACCCTGTTAT CCTTAATGTT TTGTATGGCC CAGACGAC	250 CCC CCC
50	mCEA(6D) mCEA(6D,1st&2nd)	1251 CACCATTTCC CCCTCATACA CCTATTACCG TCCAGGGGTG AACCTCAC AACTATATCT CCATCATACA CCTACTACCG TCCCGGCGTG AACTTGAC	300 GCC GCC

FIGURE 2C

5	mCEA(6D) mCEA(6D,1st&2nd)	1301 TCTCCTGCCA T <u>T</u> TC <u>T</u> TGCCA	TGCAGCCTCT TGCAGCATCC	AACCCACCTG AACCCCCCTG	CACAGTATTC CACAGTA <u>C</u> TC	1350 TIGGCTGATT CTGGCTGATT
3	mCEA(6D) mCEA(6D,1st&2nd)	1351 GATGGGAACA GATGG <u>A</u> AACA	TCCAGCAACA T <u>T</u> CAGCA <u>G</u> CA	CACACAAGAG TACTCAAGAG	CTCTTTATCT TTATTTATAA	1400 CCAACATCAC GCAACAT <u>A</u> AC
10	mCEA(6D) mCEA(6D,1st&2nd)	1401 TGAGAAGAAC TGAGAAGAAC	AGCGGACTCT AGCGGACTCT	ATACCTGCCA ATAC <u>T</u> TGCCA	GGCCAATAAC GGCCAATAAC	1450 TCAGCCAGTG TCAGCCAGTG
15	mCEA(6D) mCEA(6D,1st&2nd)	1451 GCCACAGCAG GTCACAGCAG	GACTACAGTC GACTACAGT <u>T</u>	AAGACAATCA AA <u>A</u> ACAAT <u>A</u> A	CAGTCTCTGC CTGTTTCCGC	1500 GGAGCTGCCC GGAGCTGCCC
20	mCEA(6D) mCEA(6D,1st&2nd)				CCCGTGGAGG CCCGTGGAGG	
25	mCEA(6D) mCEA(6D,1st&2nd)	1551 TGTGGCCTTC TGTGGCCTTC	ACCTGTGAAC ACCTGTGAAC	CTGAGGCTCA CTGAGGCTCA	GAACACAACC GAACACAACC	1600 TACCTGTGGT TACCTGTGGT
۵	mCEA(6D) mCEA(6D,1st&2nd)				CCAGGCTGCA CCAGGCTGCA	
30	mCEA(6D) mCEA(6D,1st&2nd)	1651 GGCAACAGGA GGCAACAGGA	CCCTCACTCT	ATTCAATGTC ATTCAATGTC	ACAAGAAATG ACAAGAAATG	1700 ACGCAAGAGC ACGCAAGAGC
35	mCEA(6D) mCEA(6D,1st&2nd)				TGCAAACCGC TGCAAACCGC	
40	mCEA(6D) mCEA(6D,1st&2nd)				CCCCCATCAT CCCCCATCAT	
	mCEA(6D) mCEA(6D,1st&2nd)				AACCTCTCCT AACCTCTCCT	
45	mCEA(6D) mCEA(6D,1st&2nd)				TATCAATGGG TATCAATGGG	
50	mCEA(6D) mCEA(6D,1st&2nd)	1901 AACACACACA AACACACACA	AGTTCTCTTT AGTTCTCTTT	ATCGCCAAAA ATCGCCAAAA	TCACGCCAAA TCACGCCAAA	1950 TAATAACGGG TAATAACGGG

FIGURE 2D

5	mCEA(6D) mCEA(6D,1st&2nd)		 	ACTGGCCGCA ACTGGCCGCA	
10	mCEA(6D) mCEA(6D,1st&2nd)		 	AACTTCTCCT AACTTCTCCT	
	mCEA(6D) mCEA(6D,1st&2nd)		 	TGCTGGTTGG TGCTGGTTGG	
15	mCEA(6D) mCEA(6D,1st&2nd)	2101 ATATAG ATATAG			

FIGURE 3

A. Amino Acid Sequence Comparison of "Wild-Type KSA" (1) and Modified KSA (2)

- 5 1 MAPPQVLAFGLLLAAATATFAAAQEECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVIC
 - 2 MAPPQVLAPGLLLAAATATFAAAQEECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVIC
 - 1 SKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCWC
 - 2 SKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCWC

10

25

30

- 1 VNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDSKSLRTALQKEITTRYQLD
- 2 VNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDSKSLRTALQKEITTRYQLD
- 1 PKFITSILYENNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLTVN
- 15 2 PKFITSVLYENNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLTVN
 - 1 GEOLDLDPGOTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVISRKKRMA
 - 2 GEQLDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVISRKKRMA
- 20 1 KYEKAEIKEMGEMHRELNA
 - 2 KYEKAEIKEMGEMHRELNA

B. DNA Sequence of Modified KSA



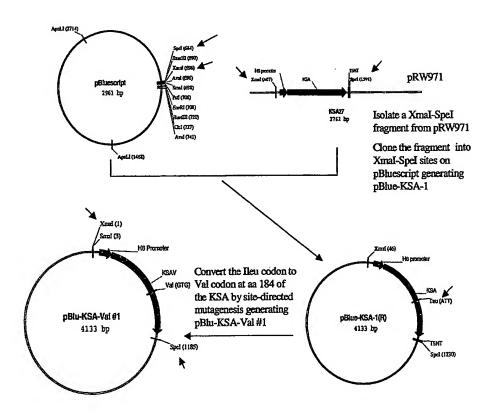


FIGURE 4B
Construction of Modified KSA Plasmid

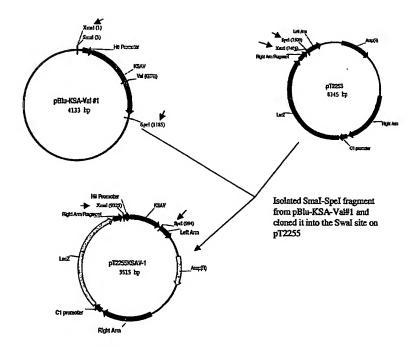
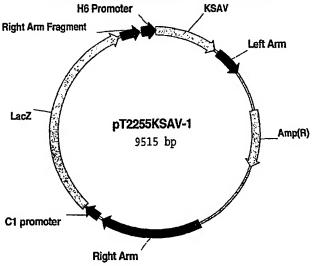


FIGURE 5

A. Plasmid Map of Modified KSA Expression Vector



5

B. DNA Sequence of Modified KSA Expression Vector

Promoter H6 for KSAV	9930-9515
KSAV	1-945
Left arm	1002-1422
Right arm	4070-5590
Right arm fragment	9012-9299

MetAlaProPro GlnValLeu AlaPheGly LeuLeuLeuAla AlaAlaThr. ATGGCGCCCC CGCAGGTCCT CGCGTTCGGG CTTCTGCTTG CCGCGGCGAC TACCGCGGGG GCGTCCAGGA GCGCAAGCCC GAAGACGAAC GGCGCCGCTG 10 .AlaThrPhe AlaAlaAlaGln GluGluCys ValCysGlu AsnTyrLysLeu· GGCGACTTTT GCCGCAGCTC AGGAAGAATG TGTCTGTGAA AACTACAAGC 51 CCGCTGAAAA CGGCGTCGAG TCCTTCTTAC ACAGACACTT TTGATGTTCG ..AlaValAsn CysPheVal AsnAsnAsnArg GlnCysGln CysThrSer TGGCCGTAAA CTGCTTTGTG AATAATAATC GTCAATGCCA GTGTACTTCA 15 101 ACCGGCATTT GACGAAACAC TTATTATTAG CAGTTACGGT CACATGAAGT ValGlyAlaGln AsnThrVal IleCysSer LysLeuAlaAla LysCysLeu 151 GTTGGTGCAC AAAATACTGT CATTTGCTCA AAGCTGGCTG CCAAATGTTT CAACCACGTG TTTTATGACA GTAAACGAGT TTCGACCGAC GGTTTACAAA .ValMetLys AlaGluMetAsn GlySerLys LeuGlyArg ArgAlaLysPro 20 201 GGTGATGAAG GCAGAAATGA ATGGCTCAAA ACTTGGGAGA AGAGCAAAAC CCACTACTTC CGTCTTTACT TACCGAGTTT TGAACCCTCT TCTCGTTTTG ..GluGlyAla LeuGlnAsn AsnAspGlyLeu TyrAspPro AspCysAsp 251 CTGAAGGGGC CCTCCAGAAC AATGATGGGC TTTATGATCC TGACTGCGAT GACTTCCCCG GGAGGTCTTG TTACTACCCG AAATACTAGG ACTGACGCTA 25 GluSerGlyLeu PheLysAla LysGlnCys AsnGlyThrSer ThrCysTrp GAGAGCGGGC TCTTTAAGGC CAAGCAGTGC AACGGCACCT CCACGTGCTG 301 CTCTCGCCCG AGAAATTCCG GTTCGTCACG TTGCCGTGGA GGTGCACGAC .CysValAsn ThrAlaGlyVal ArgArgThr AspLysAsp ThrGluIleThr 30 GTGTGTGAAC ACTGCTGGGG TCAGAAGAAC AGACAAGGAC ACTGAAATAA 351 CACACACTTG TGACGACCCC AGTCTTCTTG TCTGTTCCTG TGACTTTATT ... CysSerGlu ArgValArg ThrTyrTrpIle IleIleGlu LeuLysHis

	401	CCTGCTCTGA GCGAGTGAGA ACCTACTGGA TCATCATTGA ACTAAAACAC GGACGAGACT CGCTCACTCT TGGATGACCT AGTAGTAACT TGATTTTGTG
		LysAlaArgGlu LysProTyr AspSerLys SerLeuArgThr AlaLeuGln.
	453	AAAGCAAGAG AAAAACCTTA TGATAGTAAA AGTTTGCGGA CTGCACTTCA
_	451	TITCGTTCTC TTTTTGGAAT ACTATCATTT TCAAACGCCT GACGTGAAGT
5		LysGluIle ThrThrArgTyr GlnLeuAsp ProLysPhe IleThrSerVal
		CAAGGAGATC ACAACGCGTT ATCAACTGGA TCCAAAATTT ATCACGAGTG
	501	CTTCCTCTAG TGTTGCGCAA TAGTTGACCT AGGTTTTAAA TAGTGCTCAC
		CTTCCTCTAG TGTTGCGCAA TAGTTGACCT AGGTTTTAAA TAGTGCTCAC
		LeuTyrGlu AsnAsnVal IleThrIleAsp LeuValGln AsnSerSer
10	551	TGTTGTATGA GAATAATGTT ATCACTATTG ATCTGGTTCA AAATTCTTCT
		ACAACATACT CTTATTACAA TAGTGATAAC TAGACCAAGT TTTAAGAAGA
		GlnLysThrGln AsnAspVal AspIleAla AspValAlaTyr TyrPheGlu
	601	CAAAAAACTC AGAATGATGT GGACATAGCT GATGTGGCTT ATTATTTTGA
		GITTITITGAG TCTTACTACA CCTGTATCGA CTACACCGAA TAATAAAACT
15		.LysAspVal LysGlyGluSer LeuPheHis SerLysLys MetAspLeuThr.
	651	AAAAGATGTT AAAGGTGAAT CCTTGTTTCA TTCTAAGAAA ATGGACCTGA
		TTTTCTACAA TTTCCACTTA GGAACAAAGT AAGATTCTTT TACCTGGACT
		ValAsnGly GluGlnLeu AspLeuAspPro GlyGlnThr LeuIleTyr
	701	CAGTAAATGG GGAACAACTG GATCTGGATC CTGGTCAAAC TTTAATTTAT
20		GTCATTTACC CCTTGTTGAC CTAGACCTAG GACCAGTTTG AAATTAAATA
		TyrValAspGlu LysAlaPro GluPheSer MetGlnGlyLeu LysAlaGly.
	751	TATGTTGATG AAAAAGCACC TGAATTCTCA ATGCAGGGTC TAAAAGCTGG
		ATACAACTAC TTTTTCGTGG ACTTAAGAGT TACGTCCCAG ATTTTCGACC
	Ω.	.ValileAla ValileValVal ValValile AlaValVal AlaGlyIleVal.
25	801	TGTTATTGCT GTTATTGTGG TTGTGGTGAT AGCAGTTGTT GCTGGAATTG ACAATAACGA CAATAACACC AACACCACTA TCGTCAACAA CGACCTTAAC
		ACAATAACGA CAATAACACC AACACCACTA ICGICAACAA CGACCIIAAC
		ValleuVal IleSerArg LysLysArgMet AlaLysTyr GluLysAla TTGTGCTGGT TATTTCCAGA AAGAAGAGA TGGCAAAGTA TGAGAAGGCT
	851	AACACGACCA ATAAAGGTCT TTCTTCTCTT ACCGTTTCAT ACTCTTCCGA
20		GluIleLysGlu MetGlyGlu MetHisArg GluLeuAsnAla ***
30	007	GAGATAAAGG AGATGGGTGA GATGCATAGG GAACTCAATG CATAAGAAGC
	901	CTCTATTTCC TCTACCCACT CTACGTATCC CTTGAGTTAC GTATTCTTCG
	951	TTATCGATAC CGTCGACCTC GAGGAATTCT TTTTATTGAT TAACTAGTTA
	931	AATAGCTATG GCAGCTGGAG CTCCTTAAGA AAAATAACTA ATTGATCAAT
35	1001	ATCACGGCCG CTTATAAAGA TCTAAAATGC ATAATTTCTA AATAATGAAA
55	1001	TAGTGCCGGC GAATATITCT AGATTITACG TATTAAAGAT TTATTACTTT
	1051	AAAAAGTACA TCATGAGCAA CGCGTTAGTA TATTTTACAA TGGAGATTAA
	2002	TITTTCATGT AGTACTCGTT GCGCAATCAT ATAAAATGTT ACCTCTAATT
	1101	CGCTCTATAC CGTTCTATGT TTATTGATTC AGATGATGTT TTAGAAAAGA
40		GCGAGATATG GCAAGATACA AATAACTAAG TCTACTACAA AATCTTTTCT
	1151	AAGTTATTGA ATATGAAAAC TTTAATGAAG ATGAAGATGA CGACGATGAT
		TTCAATAACT TATACTTTTG AAATTACTTC TACTTCTACT GCTGCTACTA
	1201	TATTGTTGTA AATCTGTTTT AGATGAAGAA GATGACGCGC TAAAGTATAC
		ATAACAACAT TTAGACAAAA TCTACTTCTT CTACTGCGCG ATTTCATATG
45	1251	TATGGTTACA AAGTATAAGT CTATACTACT AATGGCGACT TGTGCAAGAA
		ATACCAATGT TTCATATTCA GATATGATGA TTACCGCTGA ACACGTTCTT
	1301	GGTATAGTAT AGTGAAAATG TTGTTAGATT ATGATTATGA AAAACCAAAT
		CCATATCATA TCACTTTTAC AACAATCTAA TACTAATACT TTTTGGTTTA
	1351	AAATCAGATC CATATCTAAA GGTATCTCCT TTGCACATAA TTTCATCTAT
50		TTTAGTCTAG GTATAGATTT CCATAGAGGA AACGTGTATT AAAGTAGATA
	1401	TCCTAGTTTA GAATACCTGC AGCCAAGCTT GGCACTGGCC GTCGTTTTAC
		AGGATCAAAT CTTATGGACG TCGGTTCGAA CCGTGACCGG CAGCAAAATG
	1451	AACGTCGTGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA
		TTGCAGCACT GACCCTTTTG GGACCGCAAT GGGTTGAATT AGCGGAACGT
55	1501	GCACATCCCC CTTTCGCCAG CTGGCGTAAT AGCGAAGAGG CCCGCACCGA
		CGTGTAGGGG GAAAGCGGTC GACCGCATTA TCGCTTCTCC GGGCGTGGCT
	1551	TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG CGCCTGATGC AGCGGGAAGG GTTGTCAACG CGTCGGACTT ACCGCTTACC GCGGACTACG
	4.504	AGCGGGAAGG GTTGTCAACG CGTCGGACTT ACCGCTTACC GCGGACTACG GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG CATATGGTGC
	1601	GGIAITITCI CCTIACGCAT CIGIGCGGIA TITCACAGCO CATALOGICO

		CC2 M2 2 2 2 C2	GGAATGCGTA	Ch ch cacath	አአአርጥርጥርርር	ርጥልጥልርርልርር
	3.653	ACTCTCAGTA	GGWWIGCGIW	TOAMOGOCOAI	TACTTARCCC	ACCCCCCACA
	1651	TGAGAGTCAT	CHAICIGCIC	ACERCOCCE	ATTANTOCC	TOCCCCCACT
		TGAGAGTCAT	CCCGCTGACG	ACTACGGCG1	CCCAMCACAC	CTCCCCCCAT
-	1701	CCCGCCAACA	GGGCGACTGC	COCCCIGACG	CCCAACACAC	CACCCCCTA
5	1001	GGGCGGTTGT	ACAAGCTGTG	ACCORDINATION OF	CCARCTCCAT	CTCTCACACC
	1751	CCGCTTACAG	TGTTCGACAC	TCCCTCTCCC	CONCONCON	CACACTOTCC
	1001	GGCGAATGTC	CATCACCGAA	ACCCCCCACACA	CCICGACGIA	TOCTCATACC
	1801	TTTTCACCGT	GTAGTGGCTT	MCGCGCGAGA	COMMINGUICC	ACCACTATICC
10	1051	AAAAGTGGCA	TAGGTTAATG	TGCGCGCICI	AATCCTTTCT	TACACTATAC
10	1851	CCTATTTTA	ATCCAATTAC	TCWICWIWWI	WAIGGIIICI	אייריייכראכייר
	7.007	GGATAAAAAT	TCGGGGAAAT	AGIACIALIA	CCCCTATTC	WICIGOWAIC
	1901	GTGGCACTTT	AGCCCCTTTA	GIGCGCGGAA	DECEMBERS	TITATITIC
•			CAAATATGTA			
1.0	1951		CAAATATGTA			
15		ATTTATGTAA	TATTGAAAAA	AGGCGAGTAC	CACHARRONA	GGACIAIIIA
	2001	GCTTCAATAA	TATIGAAAAA	GGAAGAGIAI	CHCIAIICAA	CHILICCGIG
		CGAAGTTATT	ATAACTTTTT	CCTTCTCATA	CTCATAAGTT	WITH THE TOTAL
	2051	TCGCCCTTAT	TCCCTTTTTT	GCGGCATTTT	GCCTTCCTGT	TITIGCICAC
		AGCGGGAATA	AGGGAAAAA TGGTGAAAGT	CGCCGTAAAA	COGAAGGACA	MANACCAGIG
20	2101	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAGATCAGI	ACCON COTTCC
		GGTCTTTGCG	ACCACTTTCA ATCGAACTGG	TTTTCTACGA	CTTCTAGTCA	ACCCACGIGC
	2151					
		TCACCCAATG	TAGCTTGACC	TAGAGTTGTC	GCCATTCIAG	ACIDICAL ACI
0.5	2201	TTCGCCCCGA	AGAACGTTTT TCTTGCAAAA	CCAATGATGA	GCACIIIIAA	MCDACACCIA
25		AAGCGGGGCT	TATTATCCCG	GGTTACTACT	CGIGAMAMII	TCAMGACGAT
	2251	TGTGGCGCGG	TATTATCCCG	TATTGACGCC	GGGCAAGAGC	TTCACCCACC
		ACACCGCGCC	ATAATAGGGC	ATAACTGCGG	CCCGIICICG	CCACTCACAC
	2301	CCGCATACAC	TATTCTCAGA	ATGACTIGGT	TGAGIACICA	CCMGICACAG
00		GGCGTATGTG	ATAAGAGTCT TACGGATGGC	TACTGAACCA	ACTUATGAGI	GGICAGIGIC
30	2351					
		TTTTCGTAGA	ATGCCTACCG GTGATAACAC	TACTGTCATT	CICITAATAC	CARCATCCC
•	2401	ATAACCATGA	CACTATTGTG	TGCGGCCAAC	TIACITCIGA	CHACGAICGG
	0.454	TATTGGTACT	CACTATIGIG	ACGCCGGTTG	CARGAGACI	GATCATGTAA
25	2451					CTAGTACATT
35			TCGTTGGGAA			
	2501	CTCGCCTTGA	TCGTTGGGAA	CCGGAGCTGA	WIGHNGCCNI	TGGTTTGCTG
		GAGCGGAACT	AGCAACCCTT	GGCCTCGACT	TACTICGGIA	TGCGCAAACT
	2551	GAGCGTGACA	CCACGATGCC	TGTAGCAATG	GCAACAACGI	ACGCGTTTGA
40	0.601	CTCGCACTGT	GGIGCIACGG	COCONCOUNC	CCCCCVVCVV	TTANTAGACT
40	2601	ATTAACTGGC	GAACTACTTA	CICIAGCIIC	CCGGCAACAA	TIME TAGACT
	0.554	TAATTGACCG	CITGATGAAT	GAGATCGAAG	GGCCGIIGII	AATTATCTGA GGCCCTTCCG
	2651	GGATGGAGGC	GGATAAAGTT	COMPONE	A A CA CCCCAC	CCGGGAAGGC
	0.504	CCTACCTCCG	CCTATTTCAA	CGTCCTGGTG	AAGACGCGAG	GTGGGTCTCG
45	2701	GCTGGCTGGT	TTATTGCTGA	AMMONACACOM	CCCCCTCACTCC	CACCCAGAGC
45		CGACCGACCA	AATAACGACT	ATTTAGACCT	TRANSPORTED TO THE CONTROL	CGTATCGTAG
	2751	CGGTATCATT	GCAGCACTGG	GGCCAGATGG	TAAGCCCTCC	COIMICGING
		GCCATAGTAA	CGTCGTGACC	CCGGTCTACC	MITCGGGAGG	GCHINGCAIC
	2801	TTATCTACAC	GACGGGGAGT	CAGGCAACTA	TGGATGAACG	AAATAGACAG
		AATAGATGTG	CTGCCCCTCA	GTCCGTTGAT	ACCTACTIGC	TTTATCTGTC
50	2851	ATCGCTGAGA	TAGGTGCCTC	ACTGATTAAG	CATTGGTAAC	TGTCAGACCA
		TAGCGACTCT	ATCCACGGAG	TGACTAATTC	GTAACCATTG	ACAGTCTGGT
	2901	AGTTTACTCA	TATATACTTT	AGATTGATTT	AAAACTTCAT	TTTTAATTTA
		TCAAATGAGT	ATATATGAAA	TCTAACTAAA	TTTTGAAGTA	AAAATTAAAT
	2951	AAAGGATCTA	GGTGAAGATC	CTTTTTGATA	ATCTCATGAC	CAAAATCCCT
55		TTTCCTAGAT	CCACTTCTAG	GAAAAACTAT	TAGAGTACTG	GTTTTAGGGA
	3001	TAACGTGAGT	TTTCGTTCCA	CTGAGCGTCA	GACCCCGTAG	AAAAGATCAA
		ATTGCACTCA	AAAGCAAGGT	GACTCGCAGT	CIGGGGCATC	TTTTCTAGTT
	3051	AGGATCTTCT	TGAGATCCTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCAAA
		TCCTAGAAGA	ACTCTAGGAA	AAAAAGACGC	GCATTAGACG	ACGAACGTTT

	3101	САААААААСС	ACCGCTACCA	GCGGTGGTTT	GTTTGCCGGA	TCAAGAGCTA
		GTTTTTTTGG	TGGCGATGGT	CGCCACCAAA	CAAACGGCCT	AGTTCTCGAT
	3151	CCAACTCTTT	TTCCGAAGGT	AACTGGCTTC	AGCAGAGCGC	AGATACCAAA
		GGTTGAGAAA	AAGGCTTCCA	TTGACCGAAG	TCGTCTCGCG	TCTATGGTTT
5	3201	TACTGTCCTT	CTAGTGTAGC	CGTAGTTAGG	CCACCACTTC	AAGAACTCTG
3	5	ATGACAGGAA	GATCACATCG	GCATCAATCC	GGTGGTGAAG	TTCTTGAGAC
	3251	TAGCACCGCC	TACATACCTC	GCTCTGCTAA	TCCTGTTACC	AGTGGCTGCT
	3232	ATCGTGGCGG	ATGTATGGAG	CGAGACGATT	AGGACAATGG	TCACCGACGA
	3301	CCCACTGGCG	ATAAGTCGTG	TCTTACCGGG	TTGGACTCAA	GACGATAGTT
10	3301	CCCTCACCCC	ጥልባጥሮልርሮልሮ	AGAATGGCCC	AACCTGAGTT	CTGCTATCAA
10	3351	ACCCCATAAC	CCCCACCGGT	CGGGCTGAAC	GGGGGTTCG	TGCACACAGC
	3331	ጥርርርርርጥስጥጥር	CGCGTCGCCA	GCCCGACTTG	CCCCCAAGC	ACGTGTGTCG
	3401	CCACCTTCCA	GCGAACGACC	TACACCGAAC	TGAGATACCT	ACAGCGTGAG
	2407	CCTCCAACCT	CCCTTCCTCC	ATTEMENTE	ACTCTATGGA	TGTCGCACTC
15	3451	CUNTCACANA	CCCCCACCCT	TCCCGAAGGG	AGAAAGGCGG	ACAGGTATCC
13	2421				TCTTTCCGCC	
	3501	COTARCCCCC	ACCCTCCCAA	CAGGAGAGCG	CACGAGGGAG	CTTCCAGGGG
	3301	CCATTCCCCC	ጥር ርር አርርር ሞሞ	GTCCTCTCGC	GTGCTCCCTC	GAAGGTCCCC
	3551	CONTICOCCO	CANACAMANA	ልርጥርርጥርጥርር	GGTTTCGCCA	CCTCTGACTT
20	2221	CTTTCCCCAC	CATACAAATA	TCAGGACAGC	CCAAAGCGGT	GGAGACTGAA
20	3601	CITIGCOGAC	CHIAGAMIA	CTCCTCACCC	GGGCGGAGCC	TATGGAAAA
	3001	CACCATCOAT	NANACACTAC	GAGCAGTCCC	CCCGCCTCGG	ATACCTTTTT
	3651	CICGCAGCIA	CCCCCCTTTT	TACGGTTCCT	GGCCTTTTGC	TGGCCTTTTG
	3031	CCCCTCCTTC	CCCCCCAAAA	ATGCCAAGGA	CCGGAAAACG	ACCGGAAAAC
25	3701	CTCACATCTTC	CTTTTCCTCCC	יייים יירכי ביינים	ATTCTGTGGA	TAACCGTATT
ک	3701	CACTCTACAA	GAAAGGACGC	AATAGGGGAC	TAAGACACCT	ATTGGCATAA
	3751	ACCCCCTTTC	AGTGAGCTGA	TACCGCTCGC	CGCAGCCGAA	CGACCGAGCG
	3,31	TGGCGGAAAC	TCACTCGACT	ATGGCGAGCG	GCGTCGGCTT	GCTGGCTCGC
	3801	CAGCGAGTCA	GTGAGCGAGG	AAGCGGAAGA	GCGCCCAATA	CGCAAACCGC
30	3001	GTCGCTCAGT	CACTCGCTCC	TTCGCCTTCT	CGCGGGTTAT	GCGTTTGGCG
50	3851	CTCTCCCCGC	GCGTTGGCCG	ATTCATTAAT	GCAGCTGGCA	CGACAGGTTT
	3032	GAGAGGGGGG	CGCAACCGGC	TAAGTAATTA	CGTCGACCGT	GCTGTCCAAA
	3901	CCCGACTGGA	AAGCGGGCAG	TGAGCGCAAC	GCAATTAATG	TGAGTTAGCT
	3301	GGGCTGACCT	TTCGCCCGTC	ACTCGCGTTG	CGTTAATTAC	ACTCAATCGA
35	3951	CACTCATTAG	GCACCCCAGG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT
00	5552	GTGAGTAATC	CGTGGGGTCC	GAAATGTGAA	ATACGAAGGC	CGAGCATACA
	4001	TGTGTGGAAT	TGTGAGCGGA	TAACAATTTC	ACACAGGAAA	CAGCTATGAC
		ACACACCTTA	ACACTCGCCT	ATTGTTAAAG	TGTGTCCTTT	GTCGATACTG
	4051	CATGATTACG	AATTGAATTG	CGGCCGCAAT	TCTGAATGTT	AAATGTTATA
40	•	GTACTAATGC	TTAACTTAAC	GCCGGCGTTA	AGACTTACAA	TTTACAATAT
	4101	CTTTGGATGA	AGCTATAAAT	ATGCATTGGA	AAAATAATCC	ATTTAAAGAA
		GAAACCTACT	TCGATATTTA	TACGTAACCT	TTTTATTAGG	TAAATTTCTT
	4151	AGGATTCAAA	TACTACAAAA	CCTAAGCGAT	AATATGTTAA	CTAAGCTTAT
		TCCTAAGTTT	ATGATGTTTT	GGATTCGCTA	TTATACAATT	GATTCGAATA
45	4201	TCTTAACGAC	GCTTTAAATA	TACACAAATA	AACATAATTT	TTGTATAACC
		AGAATTGCTG	CGAAATTTAT	ATGTGTTTAT	TTGTATTAAA	AACATATTGG
	4251	TAACAAATAA	CTAAAACATA	AAAATAATAA	AAGGAAATGT	AATATCGTAA
		ATTGTTTATT	GATTTTGTAT	TTTTATTATT	TTCCTTTACA	TTATAGCATT
	4301	TTATTTTACT	CAGGAATGGG	GTTAAATATT	TATATCACGT	GTATATCTAT
50		AATAAAATGA	GTCCTTACCC	CAATTTATAA	ATATAGTGCA	CATATAGATA
	4351	ACTGTTATCG	TATACTCTTT	ACAATTACTA	TTACGAATAT	GCAAGAGATA
		TGACAATAGC	ATATGAGAAA	TGTTAATGAT	AATGCTTATA	CGTTCTCTAT
	4401	ATAAGATTAC	GTATTTAAGA	GAATCTTGTC	ATGATAATTG	GGTACGACAT
		TATTCTAATG	CATAAATTCT	CTTAGAACAG	TACTATTAAC	CCATGCTGTA
55	4451	AGTGATAAAT	GCTATTTCGC	ATCGTTACAT	AAAGTCAGTT	GGAAAGATGG
	,, 	TCACTATTTA	CGATAAAGCG	TAGCAATGTA	TTTCAGTCAA	CCTTTCTACC
	4501	ATTTGACAGA	TGTAACTTAA	TAGGTGCAAA	AATGTTAAAT	AACAGCATTC
		TAAACTGTCT	ACATTGAATT	ATCCACGTTT	TTACAATTTA	TTGTCGTAAG
	4551	TATCGGAAGA	TAGGATACCA	GTTATATTAT	ACAAAAATCA	CTGGTTGGAT

		ATAGCCTTCT	ATCCTATGGT	CAATATAATA	TGTTTTTAGT	GACCAACCTA
	4601	AAAACAGATT	CTGCAATATT	CGTAAAAGAT	GAAGATTACT	GCGAATTTGT
	1001	TTTTGTCTAA	GACGTTATAA	GCATTTTCTA	CTTCTAATGA	CGCTTAAACA
	4651	AAACTATGAC	AATAAAAAGC	CATTTATCTC	AACGACATCG	TGTAATTCTT
5	1031	TTTGATACTG	TTATTTTCG	GTAAATAGAG	TTGCTGTAGC	ACATTAAGAA
•	4701	ССУЛСТТТТА	TGTATGTGTT	TCAGATATTA	TGAGATTACT	ATAAACTTTT
	1,01	GGTACAAAAT	ACATACACAA	AGTCTATAAT	ACTCTAATGA	TATTTGAAAA
	4751	TGTATACTTA	TATTCCGTAA	ACTATATTAA	TCATGAAGAA	AATGAAAAAG
	1,31	ACATATGAAT	ATAAGGCATT	TGATATAATT	AGTACTTCTT	TTACTTTTTC
10	4801	TATAGAAGCT	GTTCACGAGC	GGTTGTTGAA	AACAACAAAA	TTATACATTC
	1001	ATATCTTCGA	CAAGTGCTCG	CCAACAACTT	TTGTTGTTTT	AATATGTAAG
	4851	AAGATGGCTT	ACATATACGT	CTGTGAGGCT	ATCATGGATA	ATGACAATGC
	1001	TTCTACCGAA	TGTATATGCA	GACACTCCGA	TAGTACCTAT	TACTGTTACG
	4901	ATCTCTAAAT	AGGTTTTTGG	ACAATGGATT	CGACCCTAAC	ACGGAATATG
15	1501	TAGAGATTTA	TCCAAAAACC	TGTTACCTAA	GCTGGGATTG	TGCCTTATAC
10	4951	GTACTCTACA	ATCTCCTCTT	GAAATGGCTG	TAATGTTCAA	GAATACCGAG
	1331	CATGAGATGT	TAGAGGAGAA	CTTTACCGAC	ATTACAAGTT	CTTATGGCTC
	5001	GCTATAAAAA	TCTTGATGAG	GTATGGAGCT	AAACCTGTAG	TTACTGAATG
	3001	CCATATTTTT	AGAACTACTC	CATACCTCGA	TTTGGACATC	AATGACTTAC
20	5051	CACAACTTCT	TGTCTGCATG	ATGCGGTGTT	GAGAGACGAC	TACAAAATAG
20	3031	GTGTTGAAGA	ACAGACGTAC	TACGCCACAA	CTCTCTGCTG	ATGTTTTATC
	5101	TGAAAGATCT	GTTGAAGAAT	AACTATGTAA	ACAATGTTCT	TTACAGCGGA
	3101	ACTITIOTAGA	CAACTTCTTA	TTGATACATT	TGTTACAAGA	AATGTCGCCT
	5151	GGCTTTACTC	ChalalchChChalata	GGCAGCTTAC	CTTAACAAAG	TTAATTTGGT
25	3131	CCGAAATGAG	GAAACACAAA	CCGTCGAATG	GAATTGTTTC	AATTAAACCA
2	5201	יים ארידידיריים מייים מעמידים מעמידים	TaleColCytal	CGGCGGATGT	AGATATTTCA	AACACGGATC
	3201	ATTTGAAGAT	AACCGAGTAA	GCCGCCTACA	TCTATAAAGT	TTGTGCCTAG
	5251	GGTTAACTCC	TCTACATATA	GCCGTATCAA	ATAAAAATTT	AACAATGGTT
	3231	CCAATTGAGG	AGATGTATAT	CGGCATAGTT	TATTTTTAAA	TTGTTACCAA
30	5301	AAACTTCTAT	TGAACAAAGG	TGCTGATACT	GACTTGCTGG	ATAACATGGG
50	5501	TTTGAAGATA	ACTTGTTTCC	ACGACTATGA	CTGAACGACC	TATTGTACCC
	5351	ATGTACTCCT	TTAATGATCG	CTGTACAATC	TGGAAATATT	GAAATATGTA
	5551	TACATGAGGA	AATTACTAGC	GACATGTTAG	ACCTTTATAA	CTTTATACAT
	5401	GCACACTACT	TAAAAAAAAT	AAAATGTCCA	GAACTGGGAA	AAATTGATCT
35	020-	CGTGTGATGA	ATTTTTTTA	TTTTACAGGT	CTTGACCCTT	TTTAACTAGA
20	5451	TGCCAGCTGT	AATTCATGGT	AGAAAAGAAG	TGCTCAGGCT	ACTITICAAC
		ACGGTCGACA	TTAAGTACCA	TCTTTTCTTC	ACGAGTCCGA	TGAAAAGTTG
	5501	AAAGGAGCAG	ATGTAAACTA	CATCTTTGAA	AGAAATGGAA	AATCATATAC
	-	TTTCCTCGTC	TACATTTGAT	GTAGAAACTT	TCTTTACCTT	TTAGTATATG
40	5551	TGTTTTGGAA	TTGATTAAAG	AAAGTTACTC	TGAGACACAA	AAGAGGTAGC
		ACAAAACCTT	AACTAATTTC	TTTCAATGAG	ACTCTGTGTT	TTCTCCATCG
	5601	TGAAGTGGTA	CTCTCAAAGG	TACGTGACTA	ATTAGCTATA	AAAAGGATCC
		ACTTCACCAT	GAGAGTTTCC	ATGCACTGAT	TAATCGATAT	TTTTCCTAGG
	5651	TAGAGGATCA	TTATTTAACG	TAAACTAAAT	GGAAAAGCTA	TTTACAGGTA
45		ATCTCCTAGT	AATAAATTGC	ATTTGATTTA	CCTTTTCGAT	AAATGTCCAT
	5701	CATACGGTGT	TTTCTGGAAT	CAAATGATTC	TGATTTTGAG	GATTTTATCA
		GTATGCCACA	AAAGACCTTA	GTTTACTAAG	ACTAAAACTC	CTAAAATAGT
	5751	ATACAATAAT	GACAGTGCTA	ACTGGTAAAA	AAGAAAGCAA	ACAATTATCA
	•	TATGTTATTA	CTGTCACGAT	TGACCATTTT	TTCTTTCGTT	TGTTAATAGT
50	5801	TGGCTAACAA	TTTTTATTAT	ATTTGTAGTA	TGCATAGTGG	TCTTTACGTT
-	5552	ACCGATTGTT	AAAAATAATA	TAAACATCAT	ACGTATCACC	AGAAATGCAA
	5851	TCTTTATTTA	AAGTTAATGT	GTTAAGATTA	AATGGAGTAA	TTGGATCCCC
		AGAAATAAAT	TTCAATTACA	CAATTCTAAT	TTACCTCATT	AACCTAGGGG
	5901	CATCGATGGG	GAATTCACTG	GCCGTCGTTT	TACAACGTCG	TGACTGGGAA
55		GTAGCTACCC	CTTAAGTGAC	CGGCAGCAAA	ATGTTGCAGC	ACTGACCCTT
	5951	AACCCTGGCG	TTACCCAACT	TAATCGCCTT	GCAGCACATC	CCCCTTTCGC
	JJJ.	TTGGGACCGC	AATGGGTTGA	ATTAGCGGAA	CGTCGTGTAG	GGGGAAAGCG
	6001	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT
	0001	GTCGACCGCA	TTATCGCTTC	TCCGGGCGTG	GCTAGCGGGA	AGGGTTGTCA
		JICONCCOCK	1111100110			

		macca a caan	CARROCCCAA	Tagaaammaa	CCTGGTTTCC	CCCACCAGAA
	6051	TGCGCAGCCI	COMPACCOM	ACCCCCTTIC	GGACCAAAGG	CCCTCCTCTT
	6101	GCGGTGCCGG	AAAGCIGGCI	GGAGTGCGAT	CTTCCTGAGG	CCGAIACIGI
_		CGCCACGGCC	TTTCGACCGA	CCTCACGCTA	GAAGGACTCC	GGCIAIGACA
5	6151				TTACGATGCG	
					AATGCTACGC	
	6201				CGCCGTTTGT	
					GCGGCAAACA	
	6251	AATCCGACGG	GTTGTTACTC	GCTCACATTT	AATGTTGATG	AAAGCTGGCT
10					TTACAACTAC	
	6301				TGGCGTTAAC	
		TGTCCTTCCG	GTCTGCGCTT	AATAAAAACT	ACCGCAATTG	AGCCGCAAAG
	6351				ACGGCCAGGA	
					TGCCGGTCCT	
15	6401				CGCGCCGGAG	
		GGCAGACTTA	AACTGGACTC	GCGTAAAAAT	GCGCGGCCTC	TTTTGGCGGA
	6451	CGCGGTGATG	GTGCTGCGTT	GGAGTGACGG	CAGTTATCTG	GAAGATCAGG
		GCGCCACTAC	CACGACGCAA	CCTCACTGCC	GTCAATAGAC	CTTCTAGTCC
	6501	ATATGTGGCG	GATGAGCGGC	ATTTTCCGTG	ACGTCTCGTT	GCTGCATAAA
20		TATACACCGC	CTACTCGCCG	TAAAAGGCAC	TGCAGAGCAA	CGACGTATTT
	6551	CCGACTACAC	AAATCAGCGA	TTTCCATGTT	GCCACTCGCT	TTAATGATGA
		GGCTGATGTG	TTTAGTCGCT	AAAGGTACAA	CGGTGAGCGA	AATTACTACT
	6601				TCAGATGTGC	
		AAAGTCGGCG	CGACATGACC	TCCGACTTCA	AGTCTACACG	CCGCTCAACG
25	6651				GGCAGGGTGA	
		CACTGATGGA	TGCCCATTGT	CAAAGAAATA	CCGTCCCACT	TTGCGTCCAG
	6701	GCCAGCGGCA	CCGCGCCTTT	CGGCGGTGAA	ATTATCGATG	AGCGTGGTGG
		CGGTCGCCGT	GGCGCGGAAA	GCCGCCACTT	TAATAGCTAC	TCGCACCACC
	6751				CGTCGAAAAC	
30		AATACGGCTA	GCGCAGTGTG	ATGCAGACTT	GCAGCTTTTG	GGCTTTGACA
	6801				CGGTGGTTGA	
		CCTCGCGGCT	TTAGGGCTTA	GAGATAGCAC	GCCACCAACT	TGACGTGTGG
	6851				TGCGATGTCG	
		CGGCTGCCGT	GCGACTAACT	TCGTCTTCGG	ACGCTACAGC	CAAAGGCGCT
35	6901	GGTGCGGATT	GAAAATGGTC	TGCTGCTGCT	GAACGGCAAG	CCGTTGCTGA
					CTTGCCGTTC	
	6951	TTCGAGGCGT	TAACCGTCAC	GAGCATCATC	CTCTGCATGG	TCAGGTCATG
					GAGACGTACC	
	7001	GATGAGCAGA	CGATGGTGCA	GGATATCCTG	CTGATGAAGC	AGAACAACTT
40		CTACTCGTCT	GCTACCACGT	CCTATAGGAC	GACTACTTCG	TCTTGTTGAA
	7051	TAACGCCGTG	CGCTGTTCGC	ATTATCCGAA	CCATCCGCTG	TGGTACACGC
		ATTGCGGCAC	GCGACAAGCG	TAATAGGCTT	GGTAGGCGAC	ACCATGTGCG
	7101				ATGAAGCCAA	
		ACACGCTGGC	GATGCCGGAC	ATACACCACC	TACTTCGGTT	ATAACTTTGG
45	7151	CACGGCATGG	TGCCAATGAA	TCGTCTGACC	GATGATCCGC	GCTGGCTACC
		GTGCCGTACC	ACGGTTACTT	AGCAGACTGG	CTACTAGGCG	CGACCGATGG
	7201	GGCGATGAGC	GAACGCGTAA	CGCGAATGGT	GCAGCGCGAT	CGTAATCACC
		CCGCTACTCG	CTTGCGCATT	GCGCTTACCA	CGTCGCGCTA	GCATTAGTGG
	7251	CGAGTGTGAT	CATCTGGTCG	CTGGGGAATG	AATCAGGCCA	CGGCGCTAAT
50		GCTCACACTA	GTAGACCAGC	GACCCCTTAC	TTAGTCCGGT	GCCGCGATTA
	7301	CACGACGCGC	TGTATCGCTG	GATCAAATCT	GTCGATCCTT	CCCGCCCGGT
		GTGCTGCGCG	ACATAGCGAC	CTAGTTTAGA	CAGCTAGGAA	GGGCGGGCCA
	7351				GGCCACCGAT	
		CGTCATACTT	CCGCCGCCTC	GGCTGTGGTG	CCGGTGGCTA	TAATAAACGG
55	7401	CGATGTACGC	GCGCGTGGAT	GAAGACCAGC	CCTTCCCGGC	TGTGCCGAAA
		GCTACATGCG	CGCGCACCTA	CTTCTGGTCG	GGAAGGGCCG	ACACGGCTTT
	7451	TGGTCCATCA	AAAAATGGCT	TTCGCTACCT	GGAGAGACGC	GCCCGCTGAT
		ACCAGGTAGT	TTTTTACCGA	AAGCGATGGA	CCTCTCTGCG	CGGGCGACTA
	7501	CCTTTGCGAA	TACGCCCACG	CGATGGGTAA	CAGTCTTGGC	GGTTTCGCTA

		GGAAACGCTT	ATGCGGGTGC	GCTACCCATT	GTCAGAACCG	CCAAAGCGAT
	7551	AATACTGGCA	GGCGTTTCGT	CAGTATCCCC	GTTTACAGGG	CGGCTTCGTC
	,,,,,	TTATGACCGT	CCGCAAAGCA	GTCATAGGGG	CAAATGTCCC	GCCGAAGCAG
	7601	TEGERATUGGG	TGGATCAGTC	GCTGATTAAA	TATGATGAAA	ACGGCAACCC
5	7601	ACCCATGACCC	ACCTACTCAG	CGACTAATTT	ATACTACTT	TGCCGTTGGG
5	7651	CTCCTCCCCT	TACCCCCCCTC	ATTTTGGCGA	TACGCCGAAC	GATCGCCAGT
	1021	CACCACCCCA	ATCCCCCCAC	TAAAACCGCT	ATCCCCCTTC	CTAGCGGTCA
	7701	TOTAL TOTAL TOTAL	CCCTCTCCTC	TTTGCCGACC	GCACGCCGCA	TCCAGCGCTG
	7701	TCIGINIGAN	CCCACACCAC	AAACGGCTGG	CCTCCCCCCT	AGGTCGCGAC
10	7757	AGACATACTI	ANCACCAGCCAG	GCAGTTTTTC	CACCHCCCTT	TATCCGGGCA
10	7751	MCCCMMCCMM	MACACCAGCA	CGTCAAAAAG	CTCDAGGCAA	ATAGGCCCGT
	7007	ANGCARGGAA	CTCACCACCA	AATACCTGTT	CCCTCATAGC	CATAACCAGC
	7801	MUCCAICGAA	GIGACCAGCG	TTATGGACAA	CCCTCATATCC	CTATTGCTCG
	7851	TIGGIAGCII	CACIGGICGC	CTGGATGGTA	ACCCCCTICCC	AACCCCTCAA
15	7031	TCCTGCACTG	CHICGIGGCG	GACCTACCAT	TCCCCCACCG	TTCGCCACTT
15	7007	AGGACGTGAC	AMORGOGEOG	ACAAGGTAAA	CACMACAMAC	AVGACGAGGI
	7901	GIGCCICIGG	MACACCCACC	TGTTCCATTT	CHGIIGHIIG	TTCACCCACT
	7051	LACGGAGACC	COCCAGO	CCGGGCAACT	GICENCING	CTACCCCTAC
	7951	ACTACCGCAG	CCGGAGAGCG	GGCCCGTTGA	CIGGCICACA	CATCCCCATC
20	0007	TGATGGCGTC	GGCCICICGC	TGGTCAGAAG	CCCCCCACAT	CALCCCCTCC
20	8001	TGCAACCGAA	CGCGACCGCA	ACCAGTCTTC	CCCCCCCTCTA	CTCCCCCACC
	0.051	ACGIIGGCII	GCGCIGGCGI	AAACCTCAGT	CUCACCCATATA	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	8051			TTTGGAGTCA		
	8101			CCACCAGCGA		
25	9101	CCACGCCAIC	CCCCTACACT	GGTGGTCGCT	ጥጥአርረጥአአአአ	ACCTACCTCC
س	8151	TCCCTT ATTA	CCCTTCCCN	TTTAACCGCC	አርጥር አርርርርጥ	TCTTTCACAG
	9131	ACCCATTATA	CCCANCCCTT	AAATTGGCGG	TCAGTCCGAA	AGAAAGTGTC
	8201	ACCOMITATI	CCCATAAAA	ACAACTGCTG	ACGCCGCTGC	GCGATCAGTT
	0201	TACACCTAAC	CCCTATETTE	TGTTGACGAC	TGCGGCGACG	CGCTAGTCAA
30	8251			ACGACATTGG		
50	0231	CTCCCCTCCT	GGCGACCTAT	TGCTGTAACC	GCATTCACTT	CGCTGGGCGT
	8301	ጥጥር አር ርርሞል አ	CGCCTGGGTC	GAACGCTGGA	AGGCGGCGGG	CCATTACCAG
	0301	AACTGGGATT	GCGGACCCAG	CTTGCGACCT	TCCGCCGCCC	GGTAATGGTC
	8351	GCCGAAGCAG	CGTTGTTGCA	GTGCACGGCA	GATACACTTG	CTGATGCGGT
35	0001	CGGCTTCGTC	GCAACAACGT	CACGTGCCGT	CTATGTGAAC	GACTACGCCA
	8401	GCTGATTACG	ACCGCTCACG	CGTGGCAGCA	TCAGGGGAAA	ACCTTATTTA
	0101	CGACTAATGC	TGGCGAGTGC	GCACCGTCGT	AGTCCCCTTT	TGGAATAAAT
	8451			ATTGATGGTA		
		AGTCGGCCTT	TTGGATGGCC	TAACTACCAT	CACCAGTTTA	CCGCTAATGG
40	8501	GTTGATGTTG	AAGTGGCGAG	CGATACACCG	CATCCGGCGC	GGATTGGCCT
		CAACTACAAC	TTCACCGCTC	GCTATGTGGC	GTAGGCCGCG	CCTAACCGGA
	8551	GAACTGCCAG	CTGGCGCAGG	TAGCAGAGCG	GGTAAACTGG	CTCGGATTAG
		CTTGACGGTC	GACCGCGTCC	ATCGTCTCGC	CCATTTGACC	GAGCCTAATC
	8601	GGCCGCAAGA	AAACTATCCC	GACCGCCTTA	CTGCCGCCTG	TTTTGACCGC
45		CCGGCGTTCT	TTTGATAGGG	CTGGCGGAAT	GACGGCGGAC	AAAACTGGCG
	8651	TGGGATCTGC	CATTGTCAGA	CATGTATACC	CCGTACGTCT	TCCCGAGCGA
		ACCCTAGACG	GTAACAGTCT	GTACATATGG	GGCATGCAGA	AGGGCTCGCT
	8701	AAACGGTCTG	CGCTGCGGGA	CGCGCGAATT	GAATTATGGC	CCACACCAGT
		TTTGCCAGAC	GCGACGCCCT	GCGCGCTTAA	CTTAATACCG	GGTGTGGTCA
50	8751	GGCGCGGCGA	CTTCCAGTTC	AACATCAGCC	GCTACAGTCA	ACAGCAACTG
		CCGCGCCGCT	GAAGGTCAAG	TTGTAGTCGG	CGATGTCAGT	TGTCGTTGAC
	8801	ATGGAAACCA	GCCATCGCCA	TCTGCTGCAC	GCGGAAGAAG	GCACATGGCT
		TACCTTTGGT	CGGTAGCGGT	AGACGACGTG	CGCCTTCTTC	CGTGTACCGA
	8851	GAATATCGAC	GGTTTCCATA	TGGGGATTGG	TGGCGACGAC	TCCTGGAGCC
55		CTTATAGCTG	CCAAAGGTAT	ACCCCTAACC	ACCGCTGCTG	AGGACCTCGG
	8901	CGTCAGTATC	GGCGGAATTC	CAGCTGAGCG	CCGGTCGCTA	CCATTACCAG
		GCAGTCATAG	CCGCCTTAAG	GTCGACTCGC	GGCCAGCGAT	GGTAATGGTC
	8951	TTGGTCTGGT	GTCAAAAATA	ATAATAACCG	GGCAGGGGG	ATCCGGAGCT
		AACCAGACCA	CAGTTTTTAT	TATTATTGGC	CCGTCCCCC	TAGGCCTCGA

	9001	TATCGCAGAT	CAATGATCGC	TGTACAATCT	GGAAATATTG	AAATATGTAG
	7001	ATAGCGTCTA	GTTACTAGCG	ACATGTTAGA	CCTTTATAAC	TTTATACATC
	9051	CACACTACTT	АДАДАДАДА	AAATGTCCAG	AACTGGGAAA	AATTGATCTT
	3032	GTGTGATGAA	TTTTTTTTAT	TTTACAGGTC	TIGACCCTIT	TTAACTAGAA
5	9101	GCCAGCTGTA	ATTCATGGTA	GAAAAGAAGT	GCTCAGGCTA	CTTTTCAACA
	3202	CGGTCGACAT	TAAGTACCAT	CTTTTCTTCA	CGAGTCCGAT	GAAAAGTTGT
	9151	AAGGAGCAGA	TGTAAACTAC	ATCTTTGAAA	GAAATGGAAA	ATCATATACT
		TTCCTCGTCT	ACATTTGATG	TAGAAACTTT	CTTTACCTTT	TAGTATATGA
	9201	GTTTTGGAAT	TGATTAAAGA	AAGTTACTCT	GAGACACAAA	AGAGGTAGCT
10		CAAAACCTTA	ACTAATTTCT	TTCAATGAGA	CTCTGTGTTT	TCTCCATCGA
	9251	GAAGTGGTAC	TCTCAAAGGT	ACGTGACTAA	TTAGCTATAA	AAAGGATCCG
		CTTCACCATG	AGAGTTTCCA	TGCACTGATT	AATCGATATT	TTTCCTAGGC
	9301	GTACCCTCGA	GTCTAGAATC	GATCCCGGGT	TAATTAATTA	
		CATGGGAGCT	CAGATCTTAG	CTAGGGCCCA	TAATTAATTA	CAATAATCTG
15	9351	AAGGTGAAAA	CGAAACTATT	TGTAGCTTAA	TTAATTAGAG	CTTCTTTATT
		TTCCACTTTT	GCTTTGATAA	ACATCGAATT	AATTAATCTC	GAAGAAATAA
	9401	CTATACTTAA	AAAGTGAAAA	TAAATACAAA	GGTTCTTGAG	GGTTGTGTTA
		GATATGAATT	TTTCACTTTT	ATTTATGTTT	CCAAGAACTC	CCAACACAAT
	9451	AATTGAAAGC	GAGAAATAAT	CATAAATTAT		
20		TTAACTTTCG	CTCTTTATTA	GTATTTAATA	AAGTAATAGC	GCTATAGGCA
	9501	TAAGTTTGTA	TCGTA			
		ATTCAAACAT	AGCAT			

FIGURE 6

